



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 130647

TO: Bao-Qun Li
Location: REM/3C18
Art Unit: 1648
Thursday, August 26, 2004

Case Serial Number: 10/016986

From: Alex Waclawiw
Location: Biotech-Chem Library
Rem 1A71
Phone: 272-2534

Alexandra.waclawiw@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

From: Li, Bao-Qun
Sent: Tuesday, August 24, 2004 4:13 PM
To: STIC-Biotech/ChemLib

Please do the sequence homology and interference search for SEQ ID NO: 155 of Application SN. 10,016,986. Bao Qun Li
Art Unit 1648
Tel. 20904.
REM, 3C18.

RECEIVED
AUG 24 2004
STIC

Point of Contact:

Alexandra Wacławiw

Technical Info. Specialist

CM1 6A02 Tel: 308-449

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 8-26
Date Completed: 8-26
Searcher Prep/Rev. Time: 15
Online Time: 15

Type of Search

NA Sequence: # _____
AA Sequence: # 2
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): Cooper

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:36:03 ; Search time 13.7778 Seconds

(without alignments)

464.634 Million cell updates/sec

Title: US-10-016-986-66
Perfect score: 674
Sequence: 1 LEQSGAEVKKFGASVKVSCQ.....PDNYMDVMVGKGTIVVSS 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

- 1: /cgn2_6/protdata/2/1aa/5A COMB.pcp:*
- 2: /cgn2_6/protdata/2/1aa/5B COMB.pcp:*
- 3: /cgn2_6/protdata/2/1aa/6A COMB.pcp:*
- 4: /cgn2_6/protdata/2/1aa/6B COMB.pcp:*
- 5: /cgn2_6/protdata/2/1aa/PCITUS COMB.pcp:*
- 6: /cgn2_6/protdata/2/1aa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	674	100.0	124	1	US-08-276-852-66
2	674	100.0	124	1	US-08-899-575-66
3	674	100.0	124	1	US-08-899-575-66
4	674	100.0	124	3	US-08-591-632-1
5	674	100.0	124	4	US-09-611-451-1
6	674	100.0	124	5	PCT-US95-08743-66
7	667	99.0	146	1	US-08-276-852-155
8	667	99.0	146	1	US-08-899-575-155
9	667	99.0	146	1	US-08-899-575-155
10	667	99.0	146	5	PCT-US95-08743-155
11	664	98.5	124	3	US-08-591-632-155
12	663	98.4	124	3	US-09-611-451-45
13	663	98.4	124	3	US-08-591-632-46
14	663	98.4	124	4	US-09-611-451-46
15	660	97.9	124	1	US-08-276-852-67
16	660	97.9	124	1	US-08-899-575-67
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18	660	97.9	124	5	PCT-US95-08743-67
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22	657	97.5	124	4	US-09-611-451-49
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28	655	97.2	124	3	US-08-591-632-50
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100	527	78.2	125	1	US-08-899-575-129

ALIGNMENTS

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RESULT 1
US-08-276-852-66
; Sequence 66, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-66

Query Match 100.0%; Score 674; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSK 60
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QY 121 IVSS 124
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RESULT 2
US-08-899-575-66
; Sequence 66, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-66

Query Match 100.0%; Score 674; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 FQDRVTFADTTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 121 IVSS 124
DB 121 IVSS 124
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STIC-Biotech/ChemLib

130647

From: Li, Bao-Qun
Sent: Tuesday, August 24, 2004 4:10 PM
To: STIC-Biotech/ChemLib

Please do the sequence homology and interference search for SEQ ID NO: 66 of Application Sn. 10/016,986. Thanks.
Bao Qun LI
Art Unit 1648.
Tel. 20904.
REM, 3C18.

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-66
Query Match 100.0%; Score 674; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWNPYNGNKEFSK 60
Qy 61 FQDRVTFTADTSANTAYMELRSLSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
Db 61 FQDRVTFTADTSANTAYMELRSLSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
Qy 121 IVSS 124
Db 121 IVSS 124
RESULT 4
US-08-591-632-1
Sequence 1, Application US/08591632
Patent No. 6261558
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
Burton, Dennis R.
Lerner, Richard A.
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 92

TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,632
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11907
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-632-1
Query Match 100.0%; Score 674; DB 3; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWNPYNGNKEFSK 60
Qy 61 FQDRVTFTADTSANTAYMELRSLSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
Db 61 FQDRVTFTADTSANTAYMELRSLSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
Qy 121 IVSS 124
Db 121 IVSS 124
RESULT 5
US-09-611-451-1
Sequence 1, Application US/09611451
Patent No. 6395275
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
Burton, Dennis R.
Lerner, Richard A.
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 92

CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of
Patent Counsel
STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-611-451-1
Query Match 100.0%; Score 674; DB 4; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0
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DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINFYND
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DB 61 FQDRVTFADTTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMD
QY 121 IVSS 124
DB 121 IVSS 124
RESULT 6
PCT-US95-08743-66
Sequence 66, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743

;
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-155

Query Match 99.0%; Score 667; DB 1; Length 146;
Best Local Similarity 99.2%; Pred. No. 2.2e-60;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWNPYGNKEFSAK 82
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DB 83 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
QY 121 IVSS 124
DB 143 IVSS 146

RESULT 8
US-08-899-575-155
; Sequence 155, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-899-575-155

Query Match 99.0%; Score 667; DB 1; Length 146;
Best Local Similarity 99.2%; Pred. No. 2.2e-60;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWNPYGNKEFSAK 60
DB 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWNPYGNKEFSAK 82
QY 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 83 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
QY 121 IVSS 124
DB 143 IVSS 146

RESULT 9
US-08-899-575-155
; Sequence 155, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-155

Query Match 99.0%; Score 667; DB 1; Length 146;
Best Local Similarity 99.2%; Pred. No. 2.2e-60;

MATCHES 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHVRQAPGQRFWMGWINPYNGNKEFSK 60
 DB 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHVRQAPGQRFWMGWINPYNGNKEFSK 82

QY 61 FQDRVTTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
 DB 83 FQDRVTTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142

QY 121 IVSS 124
 DB 143 IVSS 146

RESULT 10

PCT-US95-08743-155

; Sequence 155, Application PC/TUS9508743

; GENERAL INFORMATION:

; APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

; NUMBER OF SEQUENCES: 170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/08743

; FILING DATE: 11-JUL-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/276,852

; FILING DATE: 18-JUL-1994

; INFORMATION FOR SEQ ID NO: 155:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 146 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US95-08743-155

Query Match 99.08; Score 667; DB 5; Length 146;

Best Local Similarity 99.28; Pred. No. 2.2e-60;

MATCHES 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHVRQAPGQRFWMGWINPYNGNKEFSK 60
 DB 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHVRQAPGQRFWMGWINPYNGNKEFSK 82

QY 61 FQDRVTTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
 DB 83 FQDRVTTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142

QY 121 IVSS 124
 DB 143 IVSS 146

RESULT 11

US-08-591-632-45

; Sequence 45, Application US/08591632

; Patent No. 6261558

; GENERAL INFORMATION:

; APPLICANT: Barbas, Carlos F.

; APPLICANT: Burton, Dennis R.

; APPLICANT: Lerner, Richard A.

; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL

; NUMBER OF SEQUENCES: 92

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

; ADDRESS: 10550 No. 6395275th Torrey Pines Road, TPC 8

; CITY: La Jolla

STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/591,632

FILING DATE: 19-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/11907

FILING DATE: 19-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/308,841

FILING DATE: 19-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/233,619

FILING DATE: 26-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/139,409

FILING DATE: 19-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 332.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 784-2937

TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-591-632-45

Query Match 98.58; Score 664; DB 3; Length 124;

Best Local Similarity 97.68; Pred. No. 3.7e-60;

MATCHES 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHVRQAPGQRFWMGWINPYNGNKEFSK 60
 DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHVRQAPGQRFWMGWINPYNGNKEFSK 60

QY 61 FQDRVTTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
 DB 61 FQDRVTTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 121 IVSS 124
 DB 121 IVSS 124

RESULT 12

US-09-611-451-45

; Sequence 45, Application US/0961451

; Patent No. 6395275

; GENERAL INFORMATION:

; APPLICANT: Barbas, Carlos F.

; APPLICANT: Burton, Dennis R.

; APPLICANT: Lerner, Richard A.

; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL

; NUMBER OF SEQUENCES: 92

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

; ADDRESS: 10550 No. 6395275th Torrey Pines Road, TPC 8

; CITY: La Jolla


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; STATE: CA
; COUNTRY: USA
; ZIP: 92037
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,451
; FILING DATE: 06-JUL-2000
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/591,632
; FILING DATE: 2001-10-29
;
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
;
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
;
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
;
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-611-451-45

Query Match 98.5%; Score 664; DB 4; Length 124;
Best Local Similarity 97.6%; Pred. No. 3.7e-60;
Matches 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHVWRQAPGQRFPMWGWINPYNNGKEFSAK 60
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHVWRQAPGQRFPMWGWINPYNNGKEFSAK 60
QY 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 121 IVSS 124
Db 121 IVSS 124

RESULT 13
US-08-591-632-46
; Sequence 46, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
;
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
;
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
;
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
;
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-08-591-632-46

Query Match 98.4%; Score 663; DB 3; Length 124;
Best Local Similarity 97.6%; Pred. No. 4.7e-60;
Matches 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHVWRQAPGQRFPMWGWINPYNNGKEFSAK 60
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHVWRQAPGQRFPMWGWINPYNNGKEFSAK 60
QY 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 121 IVSS 124
Db 121 IVSS 124

RESULT 14
US-09-611-451-46
; Sequence 46, Application US/09611451
; Patent No. 6395275
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,451
; FILING DATE: 06-JUL-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/591,632
; FILING DATE: 2001-10-29
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
;
; US-09-611-451-46
;
; Query Match 98.4%; Score 663; DB 4; Length 124;
; Best Local Similarity 97.6%; Pred. No. 4.7e-60;
; Matches 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGWNPYNGKFSK 60
; DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGWNPYNGKFSK 60
;
; QY 61 FQDRVTFTADTSANTAYMELRSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGT 120
; DB 61 FQDRVTFTADTSANTAYMELRSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGT 120
;
; QY 121 IVSS 124
; DB 121 IVSS 124
;
; RESULT 15
; US-08-276-852-67
; Sequence 67, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 562138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
;
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,451
; FILING DATE: 06-JUL-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/591,632
; FILING DATE: 2001-10-29
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
;
; US-09-611-451-46
;
; Query Match 98.4%; Score 663; DB 4; Length 124;
; Best Local Similarity 97.6%; Pred. No. 4.7e-60;
; Matches 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGWNPYNGKFSK 60
; DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGWNPYNGKFSK 60
;
; QY 61 FQDRVTFTADTSANTAYMELRSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGT 120
; DB 61 FQDRVTFTADTSANTAYMELRSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGT 120
;
; QY 121 IVSS 124
; DB 121 IVSS 124
;
; RESULT 15
; US-08-276-852-67
; Sequence 67, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 562138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
;
;
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-67
;
; Query Match 97.9%; Score 660; DB 1; Length 124;
; Best Local Similarity 96.8%; Pred. No. 9.4e-60;
; Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGWNPYNGKFSK 60
; DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGWNPYNGKFSK 60
;
; QY 61 FQDRVTFTADTSANTAYMELRSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGT 120
; DB 61 FQDRVTFTADTSANTAYMELRSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGT 120
;
; QY 121 IVSS 124
; DB 121 IVSS 124
;
; RESULT 16
; US-08-899-575-67
; Sequence 67, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,451
; FILING DATE: 08-JUL-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/591,632
; FILING DATE: 2001-10-29
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-611-451-46

Query Match          98.4%; Score 663; DB 4; Length 124;
Best Local Similarity 97.6%; Pred. No. 4.7e-60;
Matches 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAPGQRFPMWGWINPYNKKEFSAK 60
Db      1 LEQSGAEVKKPGASVKVSQCASGYRFSHTLHWVRQAPGQRFPMWGWINPYNKKEFSAK 60
QY      61 FQDRVTFTADTSANTAYMELRLSRSADTAVYYCARVGPSYSDDSFDQNYMDVWGKGTTV 120
Db      61 FQDRVTFTADTSANTAYMELRLSRSADTAVYYCARVGPSYSDDSFDQNYMDVWGKGTTV 120
QY      121 IVSS 124
Db      121 IVSS 124

RESULT 15
US-08-276-852-67
; Sequence 67, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 562138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,451
; FILING DATE: 08-JUL-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/591,632
; FILING DATE: 2001-10-29
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-611-451-46

Query Match          98.4%; Score 663; DB 4; Length 124;
Best Local Similarity 97.6%; Pred. No. 4.7e-60;
Matches 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAPGQRFPMWGWINPYNKKEFSAK 60
Db      1 LEQSGAEVKKPGASVKVSQCASGYRFSHTLHWVRQAPGQRFPMWGWINPYNKKEFSAK 60
QY      61 FQDRVTFTADTSANTAYMELRLSRSADTAVYYCARVGPSYSDDSFDQNYMDVWGKGTTV 120
Db      61 FQDRVTFTADTSANTAYMELRLSRSADTAVYYCARVGPSYSDDSFDQNYMDVWGKGTTV 120
QY      121 IVSS 124
Db      121 IVSS 124

RESULT 16
US-08-899-575-67
; Sequence 67, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 577040th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994

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; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-67

Query Match          97.9%; Score 660; DB 1; Length 124;
Best Local Similarity 96.8%; Pred. No. 9.4e-60;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWMGWINPYNGNKEFSK 60
   |||||
Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWMGWINPYNGNKEFSK 60
   |||||
QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYNDVWGKGT 120
   |||||
Db 61 FQDRVTFDTADTSANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYNDVWGKGT 120
   |||||
QY 121 IVSS 124
   |||||
Db 121 IVSS 124
   |||||

RESULT 17
US-08-899-575-67
; Sequence 67, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148

; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-67

Query Match          97.9%; Score 660; DB 1; Length 124;
Best Local Similarity 96.8%; Pred. No. 9.4e-60;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWMGWINPYNGNKEFSK 60
   |||||
Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWMGWINPYNGNKEFSK 60
   |||||
QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYNDVWGKGT 120
   |||||
Db 61 FQDRVTFDTADTSANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYNDVWGKGT 120
   |||||
QY 121 IVSS 124
   |||||
Db 121 IVSS 124
   |||||

RESULT 18
PCT-US95-08743-67
; Sequence 67, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPC)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-67

Query Match          97.9%; Score 660; DB 5; Length 124;
Best Local Similarity 96.8%; Pred. No. 9.4e-60;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWMGWINPYNGNKEFSK 60
   |||||
Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWMGWINPYNGNKEFSK 60
   |||||
QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYNDVWGKGT 120
   |||||
Db 61 FQDRVTFDTADTSANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYNDVWGKGT 120
   |||||
QY 121 IVSS 124
   |||||
Db 121 IVSS 124
   |||||
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Db 121 IVSS 124
||||
RESULT 19
US-08-591-632-48
; Sequence 48, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 26-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-591-632-48
Query Match 97.5%; Score 657; DB 3; Length 124;
Best Local Similarity 96.8%; Pred. No. 1.9e-59;
Matches 120; Conservative 2; Mismatches 0; Gaps 0;
Qy 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNKKEFSK 60
Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNKKEFSK 60
Qy 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTTV 120
Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTTV 120
Qy 121 IVSS 124
Db 121 IVSS 124
||||

RESULT 20
US-08-591-632-49
; Sequence 49, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-591-632-49
Query Match 97.5%; Score 657; DB 3; Length 124;
Best Local Similarity 97.6%; Pred. No. 1.9e-59;
Matches 121; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNKKEFSK 60
Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNKKEFSK 60
Qy 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTTV 120
Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTTV 120
Qy 121 IVSS 124
Db 121 IVSS 124
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RESULT 21

US-09-611-451-48
; Sequence 48, Application US/09611451
; Patent No. 6395275
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; ; Burton, Dennis R.
; ; Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ; Patent Counsel
; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-611-451-48

Query Match 97.5%; Score 657; DB 4; Length 124;
Best Local Similarity 96.8%; Pred. No. 1.9e-59;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEEWGMWINPYNGNKEFSK 60
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEEWGMWINPYNGNKEFSK 60
QY 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 121 IVSS 124
Db 121 IVSS 124

RESULT 22

US-09-611-451-49
; Sequence 49, Application US/09611451
; Patent No. 6395275
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; ; Burton, Dennis R.
; ; Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ; Patent Counsel
; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-611-451-49

Query Match 97.5%; Score 657; DB 4; Length 124;
Best Local Similarity 96.8%; Pred. No. 1.9e-59;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEEWGMWINPYNGNKEFSK 60
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEEWGMWINPYNGNKEFSK 60
QY 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 121 IVSS 124
Db 121 IVSS 124

RESULT 23

US-08-276-852-68
; Sequence 68, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R.
; ; Barbas, Carlos F.
; ; Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ; Patent Counsel
; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-611-451-49

Query Match 97.5%; Score 657; DB 4; Length 124;
Best Local Similarity 96.8%; Pred. No. 1.9e-59;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEEWGMWINPYNGNKEFSK 60
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEEWGMWINPYNGNKEFSK 60
QY 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 121 IVSS 124
Db 121 IVSS 124

RESULT 24

US-08-276-852-68
; Sequence 68, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R.
; ; Barbas, Carlos F.
; ; Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ; Patent Counsel
; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-611-451-49

Query Match 97.5%; Score 657; DB 4; Length 124;
Best Local Similarity 96.8%; Pred. No. 1.9e-59;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEEWGMWINPYNGNKEFSK 60
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEEWGMWINPYNGNKEFSK 60
QY 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 121 IVSS 124
Db 121 IVSS 124

RESULT 25

US-08-276-852-68
; Sequence 68, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R.
; ; Barbas, Carlos F.
; ; Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ; Patent Counsel
; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-611-451-49

Query Match 97.5%; Score 657; DB 4; Length 124;
Best Local Similarity 96.8%; Pred. No. 1.9e-59;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEEWGMWINPYNGNKEFSK 60
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEEWGMWINPYNGNKEFSK 60
QY 61 FQDRVTFTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
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QY 121 IVSS 124
Db 121 IVSS 124

;; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
;; NUMBER OF SEQUENCES: 170
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: The Scripps Research Institute, Office of
;; ADDRESSEE: Patent Counsel
;; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/276,852
;; FILING DATE: 18-JUL-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/178,302
;; FILING DATE: 30-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/954,148
;; FILING DATE: 30-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: SCR1452P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-554-2937
;; TELEFAX: 619-554-6312
;; INFORMATION FOR SEQ ID NO: 68:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 124 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-276-852-68

Query Match 97.3%; Score 656; DB 1; Length 124;
Best Local Similarity 96.0%; Pred. No. 2.4e-59;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQCSAGYRFSNFIHWVRQAPGQRFWMGWINPYNGKKEFSAK 60
Db 1 LEQSGAEVKKPGASVKVSQCSAGYRFSNFIHWVRQAPGQRFWMGWINPYNGKKEFSAK 60

QY 61 FQDRVTFADTSDANTAYMELRSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db 61 FQDRVTFADTSDANTAYMELRSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 121 IVSS 124
Db 121 IVSS 124

RESULT 24
US-08-899-575-68
; Sequence 68, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel

;; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
;; STREET: Mail Drop TPC8
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/899,575
;; FILING DATE: 24-JUL-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/276,852
;; FILING DATE: 18-JUL-1994
;; APPLICATION NUMBER: US 08/178,302
;; FILING DATE: 30-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/954,148
;; FILING DATE: 30-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: SCR1452P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-554-2937
;; TELEFAX: 619-554-6312
;; INFORMATION FOR SEQ ID NO: 68:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 124 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-899-575-68

Query Match 97.3%; Score 656; DB 1; Length 124;
Best Local Similarity 96.0%; Pred. No. 2.4e-59;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQCSAGYRFSNFIHWVRQAPGQRFWMGWINPYNGKKEFSAK 60
Db 1 LEQSGAEVKKPGASVKVSQCSAGYRFSNFIHWVRQAPGQRFWMGWINPYNGKKEFSAK 60

QY 61 FQDRVTFADTSDANTAYMELRSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
Db 61 FQDRVTFADTSDANTAYMELRSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 121 IVSS 124
Db 121 IVSS 124

RESULT 25
US-08-899-575-68
; Sequence 68, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA

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/
/ COUNTRY: USA
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA: US/08/899,575
/ APPLICATION NUMBER: US/08/899,575
/ FILING DATE: 24-JUL-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/276,852
/ FILING DATE: 18-JUL-1994
/ APPLICATION NUMBER: US 08/178,302
/ FILING DATE: 30-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/954,148
/ FILING DATE: 30-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: SCRI452P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 68:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 124 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-899-575-68

Query Match          97.3%; Score 656; DB 1; Length 124;
Best Local Similarity 96.0%; Pred. No. 2.4e-59;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFVWGMWINPYNKKEFSK 60
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFVWGMWINPYNKKEFSK 60
QY 61 FQDRVTFADTANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGT 120
Db 61 FQDRVTFADTANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGT 120
QY 121 IVSS 124
Db 121 IVSS 124

RESULT 26
PCT-US95-08743-68
Sequence 68, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
REFERENCE/DOCKET NUMBER: 34,163
REGISTRATION NUMBER: 34,163
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
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/
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US95-08743-68

Query Match          97.3%; Score 656; DB 5; Length 124;
Best Local Similarity 96.0%; Pred. No. 2.4e-59;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFVWGMWINPYNKKEFSK 60
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFVWGMWINPYNKKEFSK 60
QY 61 FQDRVTFADTANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGT 120
Db 61 FQDRVTFADTANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGT 120
QY 121 IVSS 124
Db 121 IVSS 124

RESULT 27
US-08-591-632-47
Sequence 47, Application US/08591632
Patent No. 6261558
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,632
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11907
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Qy	1	LEQSGAEVKKPGASVKVSQCSGYFSPSFTHWVQAQPGQGFPEHWGMINPYNCKPSAK	60
Db	1	LEQSGAEVKKPGASVKVSQCSGYFSPSFTHWVQAQPGQGFPEHWGMINPYNCKPSAK	60
Qy	61	FDQRTVFTADTSANTAYVELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTTV	120
Db	61	FDQRTVFTADTSANTAYVELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTTV	120
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Db	121	IVSS 124	

RESULT 30

RESULT 30
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 ; Sequence 50, Application US/09611451
 ; Patent No. 6395275
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbas, Carlos F.
 ; Burton, Dennis R.
 ; Berner, Richard A.
 ;
 ; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
 ; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
 ;
 ; NUMBER OF SEQUENCES: 92
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/611,451
 ; FILING DATE: 06-Jul-2000
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/591,632
 ; FILING DATE: 2001-10-29
 ; APPLICATION NUMBER: US 08/308,841
 ; FILING DATE: 19-SEP-1994
 ; APPLICATION NUMBER: US 08/233,619
 ; FILING DATE: 26-APR-1994
 ; APPLICATION NUMBER: US 08/139,409
 ; FILING DATE: 19-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: TSRI 332.3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 784-2937
 ; TELEFAX: (619) 784-9399
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 124 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
 US-09-611-451-50

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	Best Local Similarity	97.6%;	Pred. No. 3e-59;		
	Matches 121;	Conservative	1;	Mismatches 2;	Indels 0;
	Gaps	0;			
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Db	1	LEOSGAVKKPGASVKVSCASGYRFRNFVHWVQAPGQRF	EWGWINPYNGNKESAK	60	

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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:36:03 ; Search time 16.2222 Seconds
(without alignments)
464.634 Million cell updates/sec

Title: US-10-016-986-155
Perfect score: 793
Sequence: 1-NEWSKVELELSVTFGVHSQ.....PDNYMDVWGKTTIVSS 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued-Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	793	100.0	146	1	US-08-899-575-155 Sequence 155, App
3	793	100.0	146	1	US-08-899-575-155 Sequence 155, App
4	793	100.0	146	5	PCT-US95-08743-155 Sequence 155, App
5	667	84.1	124	1	US-08-276-852-66 Sequence 66, Appl
6	667	84.1	124	1	US-08-899-575-66 Sequence 66, Appl
7	667	84.1	124	3	US-08-591-632-1 Sequence 1, Appli
8	667	84.1	124	4	US-09-611-451-1 Sequence 1, Appli
9	667	84.1	124	5	PCT-US95-08743-66 Sequence 66, Appl
10	667	84.1	124	5	PCT-US95-08743-66 Sequence 45, Appl
11	657	82.8	124	3	US-08-591-632-45 Sequence 45, Appl
12	657	82.8	124	4	US-09-611-451-45 Sequence 46, Appl
13	656	82.7	124	3	US-08-591-632-46 Sequence 46, Appl
14	656	82.7	124	4	US-09-611-451-46 Sequence 46, Appl
15	653	82.3	124	1	US-08-276-852-67 Sequence 67, Appl
16	653	82.3	124	1	US-08-899-575-67 Sequence 67, Appl
17	653	82.3	124	1	US-08-899-575-67 Sequence 67, Appl
18	653	82.3	124	5	PCT-US95-08743-67 Sequence 67, Appl
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21	650	82.0	124	4	US-09-611-451-49 Sequence 49, Appl
22	649	81.8	124	1	US-08-276-852-68 Sequence 68, Appl
23	649	81.8	124	1	US-08-899-575-68 Sequence 68, Appl
24	649	81.8	124	1	US-08-899-575-68 Sequence 68, Appl
25	649	81.8	124	1	US-08-899-575-68 Sequence 68, Appl
26	649	81.8	124	1	PCT-US95-08743-68 Sequence 68, Appl
27	648	81.7	124	3	US-08-591-632-47 Sequence 47, Appl

28	648	81.7	124	3	US-08-591-632-50 Sequence 50, Appl
29	648	81.7	124	4	US-09-611-451-47 Sequence 47, Appl
30	648	81.7	124	4	US-09-611-451-50 Sequence 50, Appl
31	646	81.5	124	4	US-08-591-632-5 Sequence 5, Appli
32	646	81.5	124	4	US-09-611-451-5 Sequence 5, Appli
33	645	81.3	124	3	US-08-591-632-3 Sequence 3, Appli
34	645	81.3	124	4	US-09-611-451-3 Sequence 3, Appli
35	641.5	80.9	124	1	US-08-276-852-130 Sequence 130, App
36	641.5	80.9	124	1	US-08-899-575-130 Sequence 130, App
37	641.5	80.9	124	1	US-08-899-575-130 Sequence 130, App
38	641.5	80.9	124	5	PCT-US95-08743-130 Sequence 130, App
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41	622.5	78.5	123	3	US-08-591-632-4 Sequence 4, Appli
42	622.5	78.5	123	4	US-09-611-451-4 Sequence 4, Appli
43	619	78.1	124	3	US-08-591-632-60 Sequence 60, Appl
44	619	78.1	124	3	US-08-591-632-61 Sequence 61, Appl
45	619	78.1	124	4	US-09-611-451-60 Sequence 60, Appl
46	619	78.1	124	4	US-09-611-451-61 Sequence 61, Appl
47	618	77.9	124	3	US-08-591-632-59 Sequence 59, Appl
48	618	77.9	124	4	US-09-611-451-59 Sequence 59, Appl
49	612	77.2	124	3	US-08-591-632-54 Sequence 54, Appl
50	612	77.2	124	3	US-08-591-632-57 Sequence 57, Appl
51	612	77.2	124	4	US-09-611-451-54 Sequence 54, Appl
52	612	77.2	124	4	US-09-611-451-57 Sequence 57, Appl
53	611	77.0	124	3	US-08-591-632-55 Sequence 55, Appl
54	611	77.0	124	4	US-09-611-451-55 Sequence 55, Appl
55	610	76.9	124	3	US-08-591-632-56 Sequence 56, Appl
56	610	76.9	124	4	US-09-611-451-56 Sequence 56, Appl
57	610	76.9	124	4	US-09-611-451-58 Sequence 58, Appl
58	610	76.9	124	4	US-09-611-451-58 Sequence 58, Appl
59	600	75.7	124	4	US-08-591-632-91 Sequence 91, Appl
60	600	75.7	124	4	US-09-611-451-91 Sequence 91, Appl
61	599	75.5	124	3	US-08-591-632-89 Sequence 89, Appl
62	599	75.5	124	3	US-08-591-632-92 Sequence 92, Appl
63	599	75.5	124	4	US-09-611-451-89 Sequence 89, Appl
64	599	75.5	124	4	US-09-611-451-92 Sequence 92, Appl
65	598	75.4	124	3	US-08-591-632-90 Sequence 90, Appl
66	598	75.4	124	4	US-09-611-451-90 Sequence 90, Appl
67	572.5	72.2	124	1	US-08-276-852-126 Sequence 126, App
68	572.5	72.2	124	1	US-08-899-575-126 Sequence 126, App
69	572.5	72.2	124	1	US-08-899-575-126 Sequence 126, App
70	572.5	72.2	124	5	PCT-US95-08743-126 Sequence 125, App
71	549.5	69.3	124	1	US-08-276-852-125 Sequence 125, App
72	549.5	69.3	124	1	US-08-276-852-131 Sequence 131, App
73	549.5	69.3	124	1	US-08-899-575-125 Sequence 125, App
74	549.5	69.3	124	1	US-08-899-575-131 Sequence 131, App
75	549.5	69.3	124	1	US-08-899-575-125 Sequence 125, App
76	549.5	69.3	124	1	US-08-899-575-131 Sequence 131, App
77	549.5	69.3	124	5	PCT-US95-08743-125 Sequence 125, App
78	549.5	69.3	124	5	PCT-US95-08743-131 Sequence 131, App
79	543.5	68.5	125	1	US-08-276-852-124 Sequence 124, App
80	543.5	68.5	125	1	US-08-276-852-128 Sequence 128, App
81	543.5	68.5	125	1	US-08-899-575-124 Sequence 124, App
82	543.5	68.5	125	1	US-08-899-575-128 Sequence 128, App
83	543.5	68.5	125	1	US-08-899-575-124 Sequence 124, App
84	543.5	68.5	125	1	US-08-899-575-128 Sequence 128, App
85	543.5	68.5	125	5	PCT-US95-08743-124 Sequence 124, App
86	543.5	68.5	125	5	PCT-US95-08743-128 Sequence 128, App
87	540.5	68.2	124	1	US-08-276-852-127 Sequence 127, App
88	540.5	68.2	124	1	US-08-899-575-127 Sequence 127, App
89	540.5	68.2	124	1	US-08-899-575-127 Sequence 127, App
90	540.5	68.2	124	5	PCT-US95-08743-127 Sequence 123, App
91	536.5	67.7	126	1	US-08-276-852-123 Sequence 123, App
92	536.5	67.7	126	1	US-08-899-575-123 Sequence 123, App
93	536.5	67.7	126	1	US-08-899-575-123 Sequence 123, App
94	536.5	67.7	126	5	PCT-US95-08743-123 Sequence 132, App
95	533.5	67.3	124	1	US-08-276-852-132 Sequence 132, App
96	533.5	67.3	124	1	US-08-899-575-132 Sequence 132, App
97	533.5	67.3	124	1	US-08-899-575-132 Sequence 132, App
98	533.5	67.3	124	5	PCT-US95-08743-132 Sequence 132, App
99	528.5	66.6	139	1	US-08-253-877C-19 Sequence 19, Appl
100	528.5	66.6	139	2	US-08-452-164A-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-276-852-155
; Sequence 155, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-155

Query Match: 100.0%; Score 793; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEWSWFLFFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSCKASQYRFSNFIHWVRQAP 60
Db 1 MEWSWFLFFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSCKASQYRFSNFIHWVRQAP 60

QY 61 GQRFEMWGINPYNGNKEFSKQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGP 120
Db 61 GQRFEMWGINPYNGNKEFSKQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGP 120

QY 121 YSWDDSPQDNYMDVWGKGTIVSS 146
Db 121 YSWDDSPQDNYMDVWGKGTIVSS 146

RESULT 2
US-08-899-575-155
; Sequence 155, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-155

Query Match: 100.0%; Score 793; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEWSWFLFFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSCKASQYRFSNFIHWVRQAP 60
Db 1 MEWSWFLFFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSCKASQYRFSNFIHWVRQAP 60

QY 61 GQRFEMWGINPYNGNKEFSKQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGP 120
Db 61 GQRFEMWGINPYNGNKEFSKQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGP 120

QY 121 YSWDDSPQDNYMDVWGKGTIVSS 146
Db 121 YSWDDSPQDNYMDVWGKGTIVSS 146

APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-155

Query Match 100.0%; Score 793; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEWSWVFLFSLVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 MEWSWVFLFSLVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Qy 61 GORFEWMGWINPYNGKKEFSAKFDQVTFDTADTSANTAYMELSLRSADTAVYICARVGP 120
Db 61 GORFEWMGWINPYNGKKEFSAKFDQVTFDTADTSANTAYMELSLRSADTAVYICARVGP 120
Qy 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
Db 121 YSWDDSPQDNYMDVWGKGTIVVSS 146

RESULT 4
PCT-US95-08743-155
Sequence 155, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-155

Query Match 100.0%; Score 793; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.3e-71;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEWSWVFLFSLVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 MEWSWVFLFSLVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Qy 61 GORFEWMGWINPYNGKKEFSAKFDQVTFDTADTSANTAYMELSLRSADTAVYICARVGP 120
Db 61 GORFEWMGWINPYNGKKEFSAKFDQVTFDTADTSANTAYMELSLRSADTAVYICARVGP 120
Qy 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
Db 121 YSWDDSPQDNYMDVWGKGTIVVSS 146

RESULT 5
US-08-276-852-66
Sequence 66, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SCRI452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-276-852-66

Query Match 84.1%; Score 667; DB 1; Length 124;
Best Local Similarity 99.2%; Pred. No. 6e-59;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSQCASGYRFSNFIHWRQAPQGRFEWGMWINPYNGNKEFSK 82
DB 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHWRQAPQGRFEWGMWINPYNGNKEFSK 60
QY 83 FQDRVTTADTSANTAYMELRSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 142
DB 61 FQDRVTTADTSANTAYMELRSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 143 IVSS 146
DB 121 IVSS 124

RESULT 6

US-08-899-575-66
Sequence 66, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-66

Query Match 84.1%; Score 667; DB 1; Length 124;
Best Local Similarity 99.2%; Pred. No. 6e-59;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSQCASGYRFSNFIHWRQAPQGRFEWGMWINPYNGNKEFSK 82
DB 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHWRQAPQGRFEWGMWINPYNGNKEFSK 60
QY 83 FQDRVTTADTSANTAYMELRSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 142
DB 61 FQDRVTTADTSANTAYMELRSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 143 IVSS 146
DB 121 IVSS 124

RESULT 7

US-08-899-575-66
Sequence 66, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-66

Query Match 84.1%; Score 667; DB 1; Length 124;
Best Local Similarity 99.2%; Pred. No. 6e-59;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 82
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 60

QY 83 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
DB 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
DB 121 IVSS 124

RESULT 8
US-08-591-632-1
Sequence 1, Application US/08591632
Patent No. 6261558
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
Patent Counsel
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,632
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11907
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-591-632-1

Query Match 84.1%; Score 667; DB 3; Length 124;
Best Local Similarity 99.2%; Pred. No. 6e-59;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 82
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 60

QY 83 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
DB 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
DB 121 IVSS 124

RESULT 9
US-09-611-451-1
Sequence 1, Application US/09611451
Patent No. 6395275
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
Patent Counsel
STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-JUL-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-611-451-1

Query Match 84.1%; Score 667; DB 4; Length 124;
Best Local Similarity 99.2%; Pred. No. 6e-59;

Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHVRQAPGQRFEMWGWINPYNGNKEFSK 82
Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHVRQAPGQRFEMWGWINPYNGNKEFSK 60
QY 83 FQDRTVTTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142
Db 61 FQDRTVTTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 10
PCT-US95-08743-66
; Sequence 66, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08743-66

Query Match 84.1%; Score 667; DB 5; Length 124;
Best Local Similarity 99.2%; Pred. No. 6e-59;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHVRQAPGQRFEMWGWINPYNGNKEFSK 82
Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHVRQAPGQRFEMWGWINPYNGNKEFSK 60
QY 83 FQDRTVTTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142
Db 61 FQDRTVTTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 11
US-08-591-632-45
; Sequence 45, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; Patent Counsel

; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-632-45

Query Match 82.8%; Score 657; DB 3; Length 124;
Best Local Similarity 96.8%; Pred. No. 5.9e-58;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHVRQAPGQRFEMWGWINPYNGNKEFSK 82
Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHVRQAPGQRFEMWGWINPYNGNKEFSK 60
QY 83 FQDRTVTTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142
Db 61 FQDRTVTTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 143 IVSS 146
Db 121 IVSS 124
RESULT 12
US-09-611-451-45
; Sequence 45, Application US/09611451
; Patent No. 6395275
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; Patent Counsel
; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
; CITY: La Jolla

STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0
CURRENT APPLICATION DATA: US/09/611,451
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELEPHONE: (619) 784-9397
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-611-451-45

Query Match 82.8%; Score 657; DB 4; Length 124;
Best Local Similarity 96.8%; Pred. No. 5.9e-58;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWINPYNKKEFSK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWINPYNKKEFSK 60
QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGT 142
Db 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGT 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 13
US-08-591-632-46
Sequence 46, Application US/08591632
Patent No. 6261558
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
Burton, Dennis R.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of
Patent Counsel
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0
CURRENT APPLICATION DATA: US/08/591,632
APPLICATION NUMBER: US/08/591,632
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11907
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELEPHONE: (619) 784-9397
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-632-46

Query Match 82.7%; Score 656; DB 3; Length 124;
Best Local Similarity 96.8%; Pred. No. 7.4e-58;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWINPYNKKEFSK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPEWGMWINPYNKKEFSK 60
QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGT 142
Db 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGT 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 14
US-09-611-451-46
Sequence 46, Application US/09611451
Patent No. 6395275
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
Burton, Dennis R.
Lerner, Richard A.

TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of
Patent Counsel
STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US-09-611-451-46

Query Match 82.7%; Score 656; DB 4; Length 124;
Best Local Similarity 96.8%; Pred. No. 7.4e-58;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 23 LVOSGAEVKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGINPYNKKEFSK 82
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGINPYNKKEFSK 60

QY 83 FQDRVTTADTSTANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
DB 61 FQDRVTTADTSTANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
DB 121 IVSS 124

RESULT 15

US-08-276-852-67

Sequence 67: Application US/08/276852
Patent No. 562138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-67

Query Match 82.3%; Score 653; DB 1; Length 124;
Best Local Similarity 96.0%; Pred. No. 1.5e-57;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVOSGAEVKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGINPYNKKEFSK 82
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHVVRQAPGQRFEMWGINPYNKKEFSK 60

QY 83 FQDRVTTADTSTANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
DB 61 FQDRVTTADTSTANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
DB 121 IVSS 124

RESULT 16

US-08-899-575-67

Sequence 67: Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994

5804.440

APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-67

Query Match 82.3%; Score 653; DB 1; Length 124;
Best Local Similarity 96.0%; Pred. No. 1.5e-57;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFVWVGWINPYNGKFSAK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFVWVGWINPYNGKFSAK 60
QY 83 FQDRVTFDTADTSANTAYMELRSLRSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
Db 61 FQDRVTFDTADTSANTAYMELRSLRSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 17
US-08-899-575-67
Sequence 67, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148

FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-67

Query Match 82.3%; Score 653; DB 1; Length 124;
Best Local Similarity 96.0%; Pred. No. 1.5e-57;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFVWVGWINPYNGKFSAK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFVWVGWINPYNGKFSAK 60
QY 83 FQDRVTFDTADTSANTAYMELRSLRSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
Db 61 FQDRVTFDTADTSANTAYMELRSLRSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 18
PCT-US95-08743-67
Sequence 67, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-67

Query Match 82.3%; Score 653; DB 5; Length 124;
Best Local Similarity 96.0%; Pred. No. 1.5e-57;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFVWVGWINPYNGKFSAK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFVWVGWINPYNGKFSAK 60
QY 83 FQDRVTFDTADTSANTAYMELRSLRSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
Db 61 FQDRVTFDTADTSANTAYMELRSLRSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 143 IVSS 146

Db 121 IVSS 124

RESULT 19
US-08-591-632-48
; Sequence 48, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-632-48

Query Match 82.0%; Score 650; DB 3; Length 124;
Best Local Similarity 96.0%; Pred. No. 2.9e-57;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 23 LVSGAEVKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGKEFSK 82
Db 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGKEFSK 60
QY 83 FQDRVTFTADTSANTAYMELRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
Db 61 FQDRVTFTADTSANTAYMELRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 143 IVSS 146
Db 121 IVSS 124

Db 121 IVSS 124

RESULT 20
US-08-591-632-49
; Sequence 49, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-632-49

Query Match 82.0%; Score 650; DB 3; Length 124;
Best Local Similarity 96.8%; Pred. No. 2.9e-57;
Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 23 LVSGAEVKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGKEFSK 82
Db 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGKEFSK 60
QY 83 FQDRVTFTADTSANTAYMELRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
Db 61 FQDRVTFTADTSANTAYMELRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 21

US-09-611-451-48
; Sequence 48, Application US/09611451
; Patent No. 6395275
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; Lerner, Dennis R.
; Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
Patent Counsel

STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0

CURRENT APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000

PRIOR APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29

APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994

APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994

APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-9397

TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-611-451-48

Query Match 82.0%; Score 650; DB 4; Length 124;
Best Local Similarity 96.0%; Pred. No. 2.9e-57;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAPGQRFVWGMWNPYNGNKEFSK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAPGQRFVWGMWNPYNGNKEFSK 60

QY 83 FQDRVTFVTADTSANTAYMELRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 142
Db 61 FQDRVTFVTADTSANTAYMELRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
Db 121 IVSS 124

RESULT 22
US-09-611-451-49
; Sequence 49, Application US/09611451
; Patent No. 6395275

GENERAL INFORMATION:

APPLICANT: Barbas, Carlos F.
Burton, Dennis R.
Lerner, Richard A.

TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of
Patent Counsel

STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0

CURRENT APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000

PRIOR APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29

APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994

APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994

APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937

TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-611-451-49

Query Match 82.0%; Score 650; DB 4; Length 124;
Best Local Similarity 96.8%; Pred. No. 2.9e-57;
Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAPGQRFVWGMWNPYNGNKEFSK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAPGQRFVWGMWNPYNGNKEFSK 60

QY 83 FQDRVTFVTADTSANTAYMELRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 142
Db 61 FQDRVTFVTADTSANTAYMELRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
Db 121 IVSS 124

RESULT 23
US-08-276-852-68
; Sequence 68, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A

;; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
;; NUMBER OF SEQUENCES: 170
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: The Scripps Research Institute, Office of
;; ADDRESSEE: Patent Counsel
;; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/276,852
;; FILING DATE: 18-JUL-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/178,302
;; FILING DATE: 30-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/954,148
;; FILING DATE: 30-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: SCR1452P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-554-2937
;; TELEFAX: 619-554-6312
;; INFORMATION FOR SEQ ID NO: 68:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 124 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-276-852-68

Query Match 81.8%; Score 649; DB 1; Length 124;
Best Local Similarity 95.2%; Pred. No. 3.7e-57;
Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 60
QY 83 FQDRVTFTADTSANTAYMELRSLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142
Db 61 FQDRVTFTADTSANTAYMELRSLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 24
US-08-899-575-68
; Sequence 68, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel

;; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/899,575
;; FILING DATE: 24-JUL-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/276,852
;; FILING DATE: 18-JUL-1994
;; APPLICATION NUMBER: US 08/178,302
;; FILING DATE: 30-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/954,148
;; FILING DATE: 30-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: SCR1452P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-554-2937
;; TELEFAX: 619-554-6312
;; INFORMATION FOR SEQ ID NO: 68:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 124 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-899-575-68

Query Match 81.8%; Score 649; DB 1; Length 124;
Best Local Similarity 95.2%; Pred. No. 3.7e-57;
Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 60
QY 83 FQDRVTFTADTSANTAYMELRSLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142
Db 61 FQDRVTFTADTSANTAYMELRSLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 25
US-08-899-575-68
; Sequence 68, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA

MOLECULE TYPE: protein

US-08-591-632-47

Query Match 81.7%; Score 648; DB 3; Length 124;
Best Local Similarity 96.8%; Pred. No. 4.6e-57;
Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKYSQCASGYRFSNFWIHVRQAPGQRFEMWGWINPYNKKEFSAK 82
DB 1 LEQSGAEVKKPGASVKYSQCASGYRFSNFWIHVRQAPGQRFEMWGWINPYNKKEFSAK 60
QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146

DB 121 IVSS 124

RESULT 28

US-08-591-632-50
Sequence 50, Application US/08591632
Patent No. 6261558

GENERAL INFORMATION:

APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Lerner, Richard A.

TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 92

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/591,632

FILING DATE: 19-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/11907

FILING DATE: 19-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/308,841

FILING DATE: 19-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/233,619

FILING DATE: 26-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/139,409

FILING DATE: 19-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 332.3

TELEPHONE: (619) 784-2937

TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-591-632-50

Query Match 81.7%; Score 648; DB 3; Length 124;

Best Local Similarity 96.8%; Pred. No. 4.6e-57;
Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKYSQCASGYRFSNFWIHVRQAPGQRFEMWGWINPYNKKEFSAK 82
DB 1 LEQSGAEVKKPGASVKYSQCASGYRFSNFWIHVRQAPGQRFEMWGWINPYNKKEFSAK 60
QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146

DB 121 IVSS 124

RESULT 29

US-09-611-451-47

Sequence 47, Application US/09611451

Patent No. 6395275

GENERAL INFORMATION:

APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Lerner, Richard A.

TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 92

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/611,451

FILING DATE: 06-Jul-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/591,632

FILING DATE: 2001-10-29

APPLICATION NUMBER: US 08/308,841

FILING DATE: 19-SEP-1994

APPLICATION NUMBER: US 08/233,619

FILING DATE: 26-APR-1994

APPLICATION NUMBER: US 08/139,409

FILING DATE: 19-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 332.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 784-2937

TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-09-611-451-47

Query Match 81.7%; Score 648; DB 4; Length 124;

Best Local Similarity 96.8%; Pred. No. 4.6e-57;
Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGWNPYNGNKEFSAK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGWNPYNGNKEFSAK 60
QY 83 FQDRVTFADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
Db 61 FQDRVTFADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 143 IVSS 146
Db 121 IVSS 124

RESULT 30
US-09-611-451-50
; Sequence 50, Application US/09611451
; Patent No. 6395275
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; Burton, Dennis R.
; Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; Patent Counsel
; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,451
; FILING DATE: 06-Jul-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/591,632
; FILING DATE: 2001-10-29
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-611-451-50

Query Match 81.7%; Score 648; DB 4; Length 124;
Best Local Similarity 96.8%; Pred. No. 4.6e-57;
Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGWNPYNGNKEFSAK 82
Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGWNPYNGNKEFSAK 60

QY 83 FQDRVTFADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
Db 61 FQDRVTFADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 143 IVSS 146
Db 121 IVSS 124

Search completed: August 26, 2004, 13:40:28
Job time : 17.2222 secs

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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:33:57 ; Search time 32.6074 Seconds
(without alignments)
1199,858 Million cell updates/sec

Title: US-10-016-986-66

Perfect score: 674

Sequence: 1 LQSGAEVKKPGASVKVSCQ.....PDNYMVMWGKTTIVSS 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPREMBL 25:*

1: sp.archaea:*

2: sp.bacteria:*

3: sp.fungi:*

4: sp.human:*

5: sp.invertebrate:*

6: sp.mammal:*

7: sp.mhc:*

8: sp.organelle:*

9: sp.phage:*

10: sp.plant:*

11: sp.rodent:*

12: sp.virus:*

13: sp.vertibrate:*

14: sp.unclassified:*

15: sp.rvirus:*

16: sp.bacteriaph:*

17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	431	63.9	614	4	Q96GA6	Q96ga6 homo sapien
2	413.5	61.4	500	4	Q9BRV0	Q9brv0 homo sapien
3	403.5	59.9	159	4	Q96Q80	Q96q80 homo sapien
4	392	58.2	119	5	Q9GY22	Q9gy22 schistosoma
5	390	57.9	119	4	Q9UL94	Q9ul94 homo sapien
6	389.5	57.8	124	4	Q9UL92	Q9ul92 homo sapien
7	388	57.6	497	4	Q8WY24	Q8wy24 homo sapien
8	387	57.4	125	4	Q9UL95	Q9ul95 homo sapien
9	383.5	56.9	469	4	Q727P5	Q727p5 homo sapien
10	378.5	56.2	116	4	Q9UL89	Q9ul89 homo sapien
11	366.5	54.4	613	11	Q8VXC7	Q8vcx7 mus musculu
12	366	54.3	168	11	Q8VDC9	Q8vdc9 mus musculu
13	366	54.3	468	11	Q99L31	Q99l31 mus musculu
14	363	53.9	470	11	Q7TMK1	Q7tmk1 mus musculu
15	354.5	52.6	109	11	Q9JL75	Q9jl75 mus musculu
16	354.5	52.6	145	11	Q924R3	Q924r3 mus musculu

17	354	52.5	142	11	Q924Q1
18	352.5	52.3	143	11	Q924R0
19	352	52.2	144	11	Q924P5
20	348.5	51.7	143	11	Q924Q5
21	348	51.6	481	11	Q91WU1
22	347.5	51.6	145	11	Q924R4
23	347	51.5	117	11	Q9QXF0
24	347	51.5	147	11	Q925S3
25	346.5	51.4	278	11	Q921K1
26	346	51.3	117	11	Q9QXE9
27	346	51.3	150	4	Q9Y2S8
28	346	51.2	146	11	Q924Q3
29	345	51.2	489	11	Q8VXC4
30	344.5	51.1	143	11	Q91V67
31	343.5	51.0	145	11	Q924Q6
32	342.5	50.8	145	11	Q924Q7
33	342.5	50.8	145	11	Q924R1
34	342	50.7	146	11	Q924R8
35	341.5	50.7	482	11	Q8K172
36	341.5	50.7	488	11	Q8K0F2
37	340.5	50.5	241	11	Q921A6
38	339	50.3	473	11	Q9D814
39	338.5	50.2	145	11	Q924Q9
40	338	50.1	140	11	Q924P8
41	337.5	50.1	143	11	Q924R7
42	337.5	50.1	473	11	Q99125
43	336	49.9	140	11	Q924R2
44	336	49.9	484	11	Q991A6
45	335.5	49.8	141	11	Q924Q4
46	335.5	49.8	145	11	Q924P7
47	333	49.4	123	11	Q8VJ11
48	332.5	49.3	143	11	Q91VA2
49	332	49.2	480	11	Q8K0Z4
50	331.5	49.2	137	11	Q924R6
51	331.5	49.2	143	11	Q924Q0
52	329.5	48.9	118	11	Q921C4
53	328.5	48.7	488	11	Q91WR1
54	328	48.7	170	11	Q925S2
55	325.5	48.3	143	11	Q924P9
56	325	48.2	146	11	Q924Q8
57	324.5	48.1	114	11	Q9UL81
58	324	48.1	157	4	Q95978
59	322.5	47.8	136	11	Q7TPE3
60	321.5	47.7	463	11	Q91C4
61	321	47.6	142	11	Q924Q2
62	320.5	47.6	110	11	Q9UL77
63	320.5	47.6	496	4	Q96DK0
64	319.5	47.4	243	11	Q7TQM2
65	319	47.3	120	11	Q920E8
66	318.5	47.3	481	11	Q8VCV5
67	316.5	47.0	143	11	Q924P6
68	315	46.7	614	11	Q7TWT6
69	314.5	46.7	139	11	Q924R5
70	311	46.0	474	11	Q8R3H6
71	310	46.0	109	11	Q9JL85
72	308	45.7	481	11	Q91WT3
73	306.5	45.5	218	11	Q925S1
74	304	45.1	121	11	Q8CGS2
75	298	44.2	117	11	Q921C6
76	297.5	44.1	110	11	Q9UL83
77	293	43.5	479	11	Q91WP5
78	291	43.2	111	11	Q9D9B8
79	289.5	43.0	613	4	Q8WU11
80	286.5	42.5	573	4	Q8WU38
81	283.5	42.1	298	11	Q9QYF0
82	283.5	42.1	484	11	Q8VEA0
83	280	41.5	499	4	Q8NSK4
84	278	41.2	113	4	Q9UL90
85	274.5	40.7	147	4	Q9Y509
86	273	40.5	116	4	Q9UL93
87	268	39.8	482	4	Q7Z351
88	268	39.8	487	11	Q80Z17
89	268	39.8	597	4	Q96B59

Q8NCL6 homo sapien
Q9IXEL mus musculus
Q9HCCI homo sapien
Q9UL84 homo sapien
Q9IZ05 mus musculus
Q9UL71 homo sapien
Q9UL79 mus musculus
Q9Z0E7 mus musculus
Q8N4Y9 homo sapien
Q8WUX4 homo sapien
Q9BUL0 homo sapien

ALIGNMENTS

RESULT 1
Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SQ SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
DR PIR; S15590; S15590.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000005; HTHArac.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH ARAC FAMILY 1; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 614 AA; 67921 MW; 55EP536E77AA9BBB CRC64;
Query Match 63.9%; Score 431; DB 4; Length 614;
Best Local Similarity 66.1%; Pred. No. 8.6e-38;
Matches 82; Conservative 11; Mismatches 25; Indels 6; Gaps 1;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNKFEFSK 60
DB 23 LVQSGAEVMSFGASVRVSKTSGYAFHTYSLIHWVRQAPGQGLEWMGWISPSNDTRFAKK 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 83 FQDRVTITRDSNMTAYMELSLRSADTAVYICARGYSSSWDDA-----FDIWGGQTMV 136
QY 121 IVSS 124
DB 137 TVSS 140
RESULT 2
Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SQ SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
DR PIR; S15590; S15590.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000005; HTHArac.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH ARAC FAMILY 1; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
Query Match 61.4%; Score 413.5; DB 4; Length 500;
Best Local Similarity 66.4%; Pred. No. 5.2e-36;
Matches 83; Conservative 8; Mismatches 33; Indels 1; Gaps 1;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNKFEFSK 60
DB 23 LVQSGAEVMSFGASVRVSKTSGYAFHTYSLIHWVRQAPGQGLEWMGWISPSNDTRFAKK 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKTTV 119
DB 83 FQDRVTITRDSNMTAYMELSLRSADTAVYICARRYCSYSSCQNDYIYYMDVWGKTT 142

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QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNY---MDVWGKG 117
D 117
Db 83 FQGLTWTTRDTSTVTYMDLSLRSDDTAVYFCAREMEITFGGAVSKGFYIYGMVWGQG 142
D 142
QY 118 TTVIVSS 124
D 143 TTVTVSS 149
D 149

RESULT 4
Q9GYZ2 PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAY-2000 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.C., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FDF5FAGAB CRC64;

Query Match 58.2%; Score 392; DB 5; Length 119;
Best Local Similarity 60.5%; Pred. No. 1.9e-34;
Matches 75; Conservative 20; Mismatches 21; Indels 8; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAPGQRFQFWMGWINPYNGNKEFSAK 60
D 60
Db 4 LVESGAEVKKPGASVRSCKASGYTFTGYMHWVRQAPGQGLEWIGVNPISRGTYNYNQK 63
D 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTTV 120
D 120
Db 64 FQDRVTMTDKSFSTAYMELSLRSADSAVYICARY---YD----DHYCLDYWGQGTTV 115
D 115
QY 121 IVSS 124
D 124
Db 116 TVSS 119
D 119

RESULT 5
Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAPGQRFQFWMGWINPYNGNKEFSAK 60
D 60
Db 4 LVESGAEVKKPGASVKVSCKASGYTFTSSYYMHWVRQAPGQGLEWVGINFSGGTSYAK 63
D 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTTV 120
D 120
Db 64 FQDRVTMTDKSFSTAYMELSLRSADSAVYICARY---YD----DHYCLDYWGQGTTV 115
D 115
QY 121 IVSS 124
D 124
Db 116 TVSS 119
D 119

RESULT 6
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAPGQRFQFWMGWINPYNGNKEFSAK 60
D 60
Db 4 LVESGAEVKKPGASVKVSCKASGYTFTSSYYMHWVRQAPGQGLEWVGINFSGGTSYAK 63
D 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTTV 120
D 120
Db 64 FQGVMTTKDISISTAYMELSLRSDDTAVYICARGG-----GRGLWFDPMGQGTIV 115
D 115
QY 121 IVSS 124
D 124
Db 116 TVSS 119
D 119

Query Match 57.9%; Score 390; DB 4; Length 119;
Best Local Similarity 61.3%; Pred. No. 3.1e-34;
Matches 76; Conservative 12; Mismatches 28; Indels 8; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAPGQRFQFWMGWINPYNGNKEFSAK 60
D 60
Db 4 LVESGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWVGINPNSWITTYAQK 63
D 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTTV 120
D 120
Db 64 FQGVMTTKDISISTAYMELSLRSDDTAVYICARGG-----GRGLWFDPMGQGTIV 115
D 115
QY 121 IVSS 124
D 124
Db 116 TVSS 119
D 119

Query Match 57.8%; Score 389.5; DB 4; Length 124;
Best Local Similarity 61.7%; Pred. No. 3.7e-34;
Matches 79; Conservative 12; Mismatches 26; Indels 11; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAPGQRFQFWMGWINPYNGNKEFSAK 60
D 60
Db 4 LVESGAEVKKPGASVKVSCKASGYTFTSSYYMHWVRQAPGQGLEWVGINFSGGTSYAK 63
D 63
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QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARV-----VGPVSWDDSPQDNYMDVWGK 116
RT 117 GTTVIVSS 124
DB 117 GTTLTVSS 124

RESULT 7
Q8WY24 Q8WY24 PRELIMINARY; PRT; 497 AA.
AC Q8WY24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SMC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP Zeng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RA "Identification and characterization of SMC66, a Ig-like gene which is
RT down-regulated in colorectal cancer."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF283666; AAL36987.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;

Query Match 57.6%; Score 388; DB 4; Length 497;
Best Local Similarity 58.8%; Pred. No. 2.9e-33;
Matches 77; Conservative 12; Mismatches 26; Indels 16; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSQCOASGYRFSNFIHWVROAPGQRFWMGWINPYNGKKEFSK 60
DB 23 LEQSGAEVKKPGASVKVSQCOASGYRFSNFIHWVROAPGQRFWMGWINPYNGKKEFSK 82
QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARVG-----PYSWDDSPQDNYMDV 113
DB 83 FQGRVTFADTSANTAYMELSLRSADTAVYCARVG-----PDP 133
QY 114 WKGKTTIVSS 124
DB 134 WGHGTLTVSS 144

RESULT 8
Q9UL95 Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DB (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;

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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035019; AAD56255.1; -.
DR HSP; P01810; 2FBJ
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; OD3CD5C232488EAC CRC64;

Query Match 57.4%; Score 387; DB 4; Length 125;
Best Local Similarity 61.3%; Pred. No. 7e-34;
Matches 76; Conservative 14; Mismatches 32; Indels 2; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSQCOASGYRFSNFIHWVROAPGQRFWMGWINPYNGKKEFSK 60
DB 4 LVESGAEVKKPGASVKVSQCOASGYRFSNFIHWVROAPGQRFWMGWINPYNGKKEFSK 63
QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYCARVG-----PYSWDDSPQDNYMDVWGKTTV 120
DB 64 VQGRVTFADTSANTAYMELSLRSADTAVYCARVG-----DIWGQGTMTV 121
QY 121 IVSS 124
DB 122 TVSS 125

RESULT 9
QZ77P5 QZ77P5 PRELIMINARY; PRT; 469 AA.
AC QZ77P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haeh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC051328; AAH51328.1; -.

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KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51395 MW; C9D5BE12BAAP795C CRC64;

Query Match      56.9%; Score 383.5; DB 4; Length 469;
Best Local Similarity 58.1%; Pred. No. 8.2e-33;
Matches 75; Conservative 17; Mismatches 20; Indels 17; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWGMGINPYNGNKEFSAK 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 LVQSGAEVKPGASVKVSCASGTFSSYDLIWRQAPGQGLEWGMWISAHNGDTYAKR 82
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYYCA-----RVGPYSWDDSPQDNYMDVWG 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 FQGRVTMTDTSATTSYMEFSLRSDDTALFYCATKSRGQVGF-----DSWG 130
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 116 KGTIVVSS 124
Db 131 QGLTVTVSS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q9UL89 PRELIMINARY; PRT; 116 AA.
AC Q9UL89;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035025; AAD56261.1; -.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
FT NON_TER 116
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match      56.2%; Score 378.5; DB 4; Length 116;
Best Local Similarity 62.9%; Pred. No. 5.2e-33;
Matches 78; Conservative 10; Mismatches 25; Indels 11; Gaps 2;

QY 3 QSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWGMGINPYNGNKEFSAPQ 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 QSGAEVKPGSSVKVSCASGTFSSYALSWVRQAPGQGLEWGMRIPIILGIANVAQKPF 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 63 DRVTFADTSANTAYMELSLRSADTAVYYCA--RVGPYSWDDSPQDNYMDVWGKTTV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 GRVTITADKSTAYMELSLRSADTAVYYCASSNWGPY-----WFDLWGRGLTV 112
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 IVSS 124
Db 113 TVSS 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q8VCX7 PRELIMINARY; PRT; 613 AA.
ID Q8VCX7
AC Q8VCX7;
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DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN IGH-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018315; AAH18315.1; -.
DR MGD; MGI:96448; Igh-6.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match      54.4%; Score 366.5; DB 11; Length 613;
Best Local Similarity 56.8%; Pred. No. 7.7e-31;
Matches 71; Conservative 20; Mismatches 23; Indels 11; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFPEWGMGINPYNGNKEFSAK 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 LQSGAELMKPGASVKISKATGYTFSSYWIWKVQKRGHLEWIGELTSGSGSTNYNEK 82
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYYCA--RVGPYSWDDSPQDNYMDVWGKTTT 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 FKGATFTADTSSNTAYMQLSLTSEDSAVYYCARRLG-----RWYFDVWGAGTT 132
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 120 VIVSS 124
Db 133 VIVSS 137
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q8VDC9 PRELIMINARY; PRT; 168 AA.
ID Q8VDC9
AC Q8VDC9;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Anti-MOG 212 variable gamma 2a (Fragment).
GN IGG2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN 12;
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sembli P.;
RT "Targeting T cells to the CNS.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416332; CAC94867.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
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RT with cardiac myosin." ;
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206031; AAF69329.1; -.
DR PIR; S26312; S26312.
DR PIR; S26313; S26313.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 109
SQ SEQUENCE 109 AA; 12118 MW; FF65E441B3F936A6 CRC64;

Query Match 52.8%; Score 354.5; DB 11; Length 109;
Best Local Similarity 55.1%; Pred. NO. 1.9e-30;
Matches 65; Conservative 21; Mismatches 23; Indels 9; Gaps 66

Qy 7 EVKPGASVKVSCQASGYRFSNVIHVWVQAPQCFEHWGWINPYNGNKERSAKFQDRV 66
Db 1 ELVPGASVKVSKCKAGYFTISYVHWVKQKPGGLEWIGYINPYNDGTYKNEKFKGAT 60

Qy 67 FTADTSGANTAYMELRLSRGADTAVYYCARVGPYSWDDSPQDNYVDMVGKGTTV 124
Db 1 LTVSKSSATYMELSLTSEDSAVYCARDGNVYRG-----FDYNGQGTTLVSS 109

RESULT 16
Q924R3
ID Q924R3 PRELIMINARY; PRT; 145 AA.
AC Q924R3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHI86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067787; BAB63272.1; -.
DR PIR; F28833; F28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR PIR; S26744; S26744.
DR InterPro; IPR007110; Ig-like.

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Db      114 TVSS 117
||||
RESULT 18
Q924R0 PRELIMINARY; PRT; 143 AA.
AC Q924R0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHL86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB067790; BAB63275.1; -.
DR PIR: F28833; F28833.
DR PIR: F33932; F33932.
DR PIR: PH1105; PH1105.
DR PIR: PH1108; PH1108.
DR PIR: PH1114; PH1114.
DR PIR: PH1118; PH1118.
DR PIR: PH1119; PH1119.
DR PIR: PH1125; PH1125.
DR PIR: PH1126; PH1126.
DR PIR: PH1128; PH1128.
DR PIR: PH1129; PH1129.
DR PIR: PH1131; PH1131.
DR PIR: PH1134; PH1134.
DR PIR: PH1137; PH1137.
DR PIR: PH1139; PH1139.
DR PIR: PH1142; PH1142.
DR PIR: PH1144; PH1144.
DR PIR: PH1147; PH1147.
DR PIR: PH1149; PH1149.
DR PIR: PH1150; PH1150.
DR PIR: PH1151; PH1151.
DR PIR: PH1152; PH1152.
DR PIR: PH1153; PH1153.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IG_1.
DR PROSITE: PS50835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15868 MW; 139B2E966B81E07F CRC64;

Query Match 52.3%; Score 352.5; DB 11; Length 143;
Best Local Similarity 52.4%; Pred. No. 4.3e-30;
Matches 65; Conservative 26; Mismatches 24; Indels 9; Gaps 2;

Qy 1 LEQGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGKFSK 60
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 LQPGAEVLKPGASVKLSCKASGYTFTSYWVHWVKQRPGRGLEWIGRIDNSGGTKYNEK 63
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 61 FQDRVTFTADTSANTAYMELSLRSADTAVVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 FSKATLTVDKPSSTAYMQLSLTSDSAVYICAR-----WD----EDYMDYWGKTSV 114
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 121 IVSS 124
|||
Db 115 TVSS 118
||||

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RESULT 19
Q924P5 PRELIMINARY; PRT; 144 AA.
AC Q924P5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHL86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB069920; BAB63936.1; -.
DR PIR: PH1137; PH1137.
DR PIR: S26744; S26744.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IG_1.
DR PROSITE: PS50835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 144
SQ SEQUENCE 144 AA; 15865 MW; CD07BE97E95C1B27 CRC64;

Query Match 52.2%; Score 352; DB 11; Length 144;
Best Local Similarity 52.4%; Pred. No. 4.9e-30;
Matches 65; Conservative 22; Mismatches 29; Indels 8; Gaps 1;

Qy 1 LEQGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGKFSK 60
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 LQPGAEVLKPGASVKLSCKASGYTFTSYWVHWVKQRPGRGLEWIGRIDNSGGTKYNEK 63
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 61 FQDRVTFTADTSANTAYMELSLRSADTAVVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 FSKATLTVDKPSSTAYMQLSLTSDSAVYICASYGV-----YFDVWGKTTV 115
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 121 IVSS 124
|||
Db 116 TVSS 119
||||

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RESULT 20
Q924Q5 PRELIMINARY; PRT; 143 AA.
AC Q924Q5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHL86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB067795; BAB63280.1; -.
DR PIR: F28833; F28833.
DR PIR: PH1105; PH1105.

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DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15908 MW; 55A2372870F0D568 CRC64;

Query Match
Best Local Similarity 51.7%; Score 348.5; DB 11; Length 143;
Matches 65; Conservative 22; Mismatches 28; Indels 9; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 60
DB 4 LQSGAEVKKPGASVKLSCKASGYTFTSYIHWVKRPGRGLEWIGRIDPNSGGTYKNEK 63
QY 61 FQDRVTFADTASNTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 64 FRSKALTVDKPSSTAYMQLSSITSDSAVYICARFYDYE-----YFDVWGKGTIV 114
QY 121 IVSS 124
DB 115 TVSS 118

RESULT 21
Q1WT1 PRELIMINARY; PRT; 481 AA.
AC Q1WT1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC TISSUE=Color;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

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Query Match
Best Local Similarity 51.6%; Score 348; DB 11; Length 481;
Matches 65; Conservative 23; Mismatches 26; Indels 10; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 60
DB 23 LQSGPELVKPGASVKLSCKASGYTFTSYIHWVKRPGQGLVWIGWYIPGDGNTKYNK 82
QY 61 FQDRVTFADTASNTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 83 FKGKTLTADKSSSTAYMFLSSLTSDSAVYICARVGGWAF-----DYWGQGTTL 132
QY 121 IVSS 124
DB 133 TVSS 136

RESULT 22
Q24R4 PRELIMINARY; PRT; 145 AA.
AC Q24R4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067785; BAB63270.1; -.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16081 MW; ECDBIAL35E05B88AA CRC64;

Query Match
Best Local Similarity 51.6%; Score 347.5; DB 11; Length 145;
Matches 65; Conservative 23; Mismatches 26; Indels 10; Gaps 1;

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Matches 65; Conservative 25; Mismatches 27; Indels 7; Gaps 2;
QY 1 LEQSGAEVKKPGASVKVSQCOASGYRFSNFVIHWVROAPGQRFPEWMGWINPYNGNKEFSK 60
Db 4 LQPGAEVLVPGASVKLSCKASGYTTSYWMHVVKQRPFGGLEWIRIPNSGGTYKNEK 63
QY 61 FQDRVTFTADTSANTAYMELRSADTAVYVCARVGPYSWDDSPQDNYMDVWVGKGTIV 120
Db 64 FKSKATLTVDKPSSTAYMQLSLTSDSAYVCAR-SDYDYD-----YMDYWGQGTIV 116
QY 121 IVSS 124
Db 117 TVSS 120
RESULT 23
Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
QY RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ25171; CAB65236.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 117
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47B4C CRC64;
Query Match 51.5%; Score 347; DB 11; Length 117;
Best Local Similarity 51.6%; Pred. No. 1.3e-29;
Matches 64; Conservative 23; Mismatches 27; Indels 10; Gaps 1;
QY 1 LEQSGAEVKKPGASVKVSQCOASGYRFSNFVIHWVROAPGQRFPEWMGWINPYNGNKEFSK 60
Db 4 LQSGPELVKPGASVKRSCKASGYTFDYMKVVKQSHGKSLWIGDIPNNGGTSYNOK 63
QY 61 FQDRVTFTADTSANTAYMELRSADTAVYVCARVGPYSWDDSPQDNYMDVWVGKGTIV 120
Db 64 FKSKATLTVDKSSSTAYMQLSLTSDSAYVCAR-----DKDYFDYWGQGTIV 113
QY 121 IVSS 124
Db 114 TVSS 117
RESULT 24
Q925S3 PRELIMINARY; PRT; 147 AA.
AC Q925S3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
QY RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAI12207.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
Query Match 51.4%; Score 346.5; DB 11; Length 278;
Best Local Similarity 53.2%; Pred. No. 4.2e-29;
Matches 66; Conservative 21; Mismatches 30; Indels 7; Gaps 2;
QY 1 LEQSGAEVKKPGASVKVSQCOASGYRFSNFVIHWVROAPGQRFPEWMGWINPYNGNKEFSK 60
Db 23 LQPGAEVLVPGASVKLSCKASGYTTSYWMHVVKQRPFGGLEWIRIPNSGGTNYNEK 82
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RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after irradiation in mice.";
RN World J. Gastroenterol. 6:709-717(2000).
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240166; AAK43731.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;
Query Match 51.5%; Score 347; DB 11; Length 147;
Best Local Similarity 55.6%; Pred. No. 1.7e-29;
Matches 69; Conservative 17; Mismatches 30; Indels 8; Gaps 2;
QY 1 LEQSGAEVKKPGASVKVSQCOASGYRFSNFVIHWVROAPGQRFPEWMGWINPYNGNKEFSK 60
Db 6 LHQSGPELVKPGASVKLSCKASGYTTSYDIDWVROTPQEGLEWIFPGSGSTEYNEK 65
QY 61 FQDRVTFTADTSANTAYMELRSADTAVYVCARVGPYSWDDSPQDNYMDVWVGKGTIV 120
Db 66 FKGRATLVKSSSTAYMQLSLTSDSAYVCAR-CDYY-----RRFDLWGQGTIV 117
QY 121 IVSS 124
Db 118 TVSS 121
RESULT 25
Q921K1 PRELIMINARY; PRT; 278 AA.
AC Q921K1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAI12207.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
Query Match 51.4%; Score 346.5; DB 11; Length 278;
Best Local Similarity 53.2%; Pred. No. 4.2e-29;
Matches 66; Conservative 21; Mismatches 30; Indels 7; Gaps 2;
QY 1 LEQSGAEVKKPGASVKVSQCOASGYRFSNFVIHWVROAPGQRFPEWMGWINPYNGNKEFSK 60
Db 23 LQPGAEVLVPGASVKLSCKASGYTTSYWMHVVKQRPFGGLEWIRIPNSGGTNYNEK 82
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QY 61 FQDRVTFVTADTANTAYMELRLSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 83 FKNKATLAVDKSSVTVMQLSILTSSEDSAVYICTR--GIGYDD-----VYFDVWGAGTIV 135
QY 121 IVSS 124
DB 136 TVSS 139

RESULT 26
Q9QXES PRELIMINARY; PRT; 117 AA.
AC Q9QXES;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch F.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225174; CAB65237.1; -.
DR PIR; F33932; F33932.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 117
FT NON TER 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 51.3%; Score 346; DB 11; Length 117;
Best Local Similarity 52.8%; Pred. No. 1.7e-29;
Matches 66; Conservative 22; Mismatches 25; Indels 12; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSQASGYRFSNFWVHWVROAPGQRFVWGWINPYNKKEFSAK 60
DB 4 LQSGAEVKPGASVKVSQASGYRFTDYMKVKQSHKSLWGDINPNNGGTSYQK 63
QY 61 FQDRVTFVTADTANTAYMELRLSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 119
DB 64 FKGAATLVDKSSSTAYMQLSILTSSEDSAVYICAR-----DRYYAMDYWGQGTS 112
QY 120 IVSS 124
DB 113 TVSS 117

RESULT 27
Q9Y298 PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE IGG VH protein precursor (Fragment).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT IgG4 monoclonal antibody derived from a hemophilia A patient with
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inhibitor.";
RT BLOOD 92:496-506(1998).
RL EMBL; AJ224083; CAAL1829.1; -.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005887; C:Integral to plasma membrane; NAS.
DR GO; GO:0016489; F:Immunoglobulin receptor activity; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT NON TER 150 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 51.3%; Score 346; DB 4; Length 150;
Best Local Similarity 55.6%; Pred. No. 2.3e-29;
Matches 69; Conservative 15; Mismatches 30; Indels 10; Gaps 1;

QY 1 LEQSGAEVKPGASVKVSQASGYRFSNFWVHWVROAPGQRFVWGWINPYNKKEFSAK 60
DB 23 LVQSGAEVKPGASVKVSCKVSGYTLTLPVHWVQAPGKLEWGSFDESGLIARE 82
QY 61 FQDRVTFVTADTANTAYMELRLSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 83 FQGSVTMTADTSTDIAYMELSLRSDDTAVYVCAPDPAF-----DIWGQGTIV 132
QY 121 IVSS 124
DB 133 TVSS 136

RESULT 28
Q924Q3 PRELIMINARY; PRT; 146 AA.
AC Q924Q3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067797; BAB63282.1; -.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; F3105; F3105.
DR PIR; F3108; F3108.
DR PIR; F3114; F3114.
DR PIR; F3118; F3118.
DR PIR; F3119; F3119.
DR PIR; F3125; F3125.
DR PIR; F3126; F3126.
DR PIR; F3128; F3128.
DR PIR; F3129; F3129.
DR PIR; F3131; F3131.
DR PIR; F3134; F3134.
DR PIR; F3137; F3137.
DR PIR; F3139; F3139.
DR PIR; F3142; F3142.
DR PIR; F3144; F3144.
DR PIR; F3147; F3147.
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DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16136 MW; CEABDD6E1955807F CRC64;

Query Match 51.2%; Score 345; DB 11; Length 146;
Best Local Similarity 52.4%; Pred. No. 2.8e-29;
Matches 65; Conservative 25; Mismatches 28; Indels 6; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGNKEFSK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 LQPGAEELVRPETSVKLSCKASGYTFISYWHVWKQRPGRGLEWIGRIDPNSGGTKYNEK 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FQDRVTFATDSANTAYMEILRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 FKGRATLVTDTSSSTAYMQLSLTSEDSAVYICAR-SLYDYG-----YMDYWGQGTSV 117
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 IVSS 124
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Db 118 TVSS 121
   |||

RESULT 29
Q8VCX4 PRELIMINARY; PRT; 489 AA.
AC Q8VCX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Hypothetical protein.
GN IGH-VJ558 OR A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018322.1; -.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 489 AA; 53208 MW; CC85B1194DAFE2C CRC64;

Query Match 51.2%; Score 345; DB 11; Length 489;
Best Local Similarity 50.4%; Pred. No. 1.2e-28;
Matches 65; Conservative 23; Mismatches 29; Indels 12; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGNKEFSK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 LQSGAEELVRPETSVKLSCKASGYTFSDYFIHWIKQRPGRGLEWIGFNPGRSGSKYNEK 82
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FQDRVTFATDSANTAYMEILRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 FKGRATLVTDTSSSTAYMQLSLTSEDSAVYFCAR-----HEDRGNYDGSILAWFVYWG 135
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 116 KGTTVIVSS 124
   |||:|||||:
Db 136 QGTLVTVSA 144
   |||:|||||:

RESULT 30
Q91V67 PRELIMINARY; PRT; 143 AA.
AC Q91V67;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHS96.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
GN V304-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kozono Y., Kozono H., Azuma T.;
RL "Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069912; BAB63928.1; -.
DR EMBL; AB069914; BAB63930.1; -.
DR PIR; S26744; S26744.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15775 MW; 91BC6012B44EFEBF CRC64;

Query Match 51.1%; Score 344.5; DB 11; Length 143;
Best Local Similarity 51.6%; Pred. No. 3.1e-29;
Matches 64; Conservative 23; Mismatches 28; Indels 9; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNGNKEFSK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 LQPGAEELVRPETSVKLSCKASGYTFISYWHVWKQRPGRGLEWIGVIDSDSYTNQK 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FQDRVTFATDSANTAYMEILRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 FKGRATLVTDTSSSTAYMQLSLTSEDSAVYICA-----PTVDDWYFDVWGKTTV 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 IVSS 124
   |||
Db 115 TVSS 118
   |||

Search completed: August 26, 2004, 13:39:23
Job time : 38.6074 secs
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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:34:32 ; Search time 11.9407 Seconds

(without alignments)

998.912 Million cell updates/sec

Title: US-10-016-986-66

Perfect score: 674

Sequence: 1 LKQSGAEVKKPGASVKVSQ.....PDNYMDVWGKGTIVSS 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR-78:

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1.	433	67.2	129	2	S36260 Ig heavy chain V r
2	449	66.6	129	2	S46393 Ig heavy chain V r
3	433.5	64.3	118	2	PH1666 Ig heavy chain V r
4	432.5	64.2	124	2	S19665 Ig heavy chain V r
5	423.5	62.8	114	2	PH1667 Ig heavy chain V r
6	419	62.2	148	2	S29257 Ig heavy chain V r
7	417	61.9	123	2	D33548 Ig heavy chain V-1
8	416.5	61.8	118	2	S36265 Ig heavy chain V r
9	413	61.3	133	2	C33548 Ig heavy chain V-1
10	413	61.3	627	2	S14683 Ig mu chain precur
11	408	60.5	127	2	PH0955 Ig heavy chain V r
12	402.5	59.7	136	2	S31600 Ig heavy chain V r
13	402.5	59.7	143	1	ELHUND Ig heavy chain pre
14	400	59.3	122	2	S46394 Ig heavy chain V r
15	398.5	59.1	132	2	S18553 Ig heavy chain V r
16	397	58.9	117	2	S34014 Ig heavy chain V r
17	396	58.8	127	2	B33548 Ig heavy chain V r
18	395.5	58.7	136	2	PH0961 Ig heavy chain V r
19	395.5	58.7	132	2	PH0954 Ig heavy chain V-1
20	395.5	58.7	135	2	S49530 anti-Sm antibody V
21	394	58.5	121	2	A49590 Ig heavy chain V r
22	393.5	58.4	171	2	S23623 Ig heavy chain V r
23	392.5	58.2	104	2	PH1665 Ig heavy chain V r
24	392	58.2	119	2	PH0961 Ig heavy chain V r
25	390.5	57.9	120	2	S31999 Ig heavy chain V r
26	390	57.9	131	2	S26792 Ig heavy chain V r
27	389.5	57.8	122	2	PH0958 Ig heavy chain V r
28	389.5	57.8	128	2	PH0952 Ig heavy chain pre
29	386.5	57.3	135	2	B32274 Ig heavy chain pre

30	386	57.3	142	2	A32483 Ig heavy chain V r
31	386	57.3	160	2	PH0105 anti-PR2 erythrocy
32	385.5	57.3	136	2	PH0960 Ig heavy chain V r
33	385	57.1	126	2	I44151 Ig heavy chain V r
34	383.5	56.9	118	2	S38717 Ig heavy chain V r
35	383	56.8	125	2	PH0957 Ig heavy chain V r
36	383	56.8	125	2	S68170 Ig heavy chain V r
37	382.5	56.8	122	2	PH0887 Ig heavy chain V r
38	382	56.7	122	2	B49590 Ig heavy chain V r
39	381	56.5	117	2	S18552 Ig heavy chain V r
40	381	56.5	121	2	S20783 Ig heavy chain V r
41	378	56.1	98	2	S26919 Ig heavy chain V r
42	378	56.1	109	2	PH1668 Ig heavy chain V r
43	378	56.1	135	2	PH0953 Ig heavy chain V r
44	376.5	55.9	131	2	S66537 Ig heavy chain V r
45	374.5	55.6	110	2	PH1670 Ig heavy chain V r
46	374.5	55.6	116	2	PH0959 Ig heavy chain V r
47	374.5	55.6	116	2	S36261 Ig heavy chain V r
48	373	55.3	123	2	B30560 Ig heavy chain V r
49	372.5	55.3	139	2	A27609 Ig heavy chain pre
50	371	55.0	98	2	S26938 Ig heavy chain V r
51	371	55.0	117	2	S18551 Ig heavy chain V r
52	370.5	55.0	120	2	PH0862 Ig heavy chain V r
53	370	54.9	122	2	C49590 Ig heavy chain V r
54	370	54.9	246	2	S38950 Ig gamma-2a chain
55	370	54.9	446	2	S40295 Ig heavy chain V r
56	369.5	54.8	120	2	G28195 Ig heavy chain V r
57	368.5	54.7	110	2	PH1669 Ig heavy chain V r
58	368.5	54.7	128	2	C37267 Ig heavy chain V r
59	368	54.6	98	2	S26921 Ig heavy chain V r
60	368	54.6	117	2	S31680 Ig heavy chain V r
61	367	54.5	129	2	A33548 Ig heavy chain V-1
62	367	54.5	131	2	S21924 Ig heavy chain V r
63	366.5	54.4	117	2	S25176 Ig heavy chain V r
64	366.5	54.4	132	2	S31596 Ig heavy chain V r
65	365.5	54.2	120	2	F28195 Ig heavy chain V r
66	365	54.2	104	2	S69899 Ig heavy chain V r
67	364.5	54.1	128	2	A37267 Ig heavy chain V r
68	364	54.0	136	2	S04576 Ig heavy chain pre
69	363.5	53.9	241	2	S69131 Ig heavy chain (DO
70	363	53.9	98	2	S26912 Ig heavy chain V r
71	362.5	53.8	139	2	PS0024 Ig heavy chain pre
72	361.5	53.6	128	2	I37267 Ig heavy chain V r
73	361	53.6	98	2	S26920 Ig heavy chain V r
74	361	53.6	116	2	S31667 Ig heavy chain V r
75	361	53.6	117	1	HVHUHG Ig heavy chain pre
76	360	53.4	98	2	S26918 Ig heavy chain V r
77	359	53.3	116	2	S24289 Ig gamma chain V r
78	359	53.3	117	2	PT0371 Ig gamma chain pre
79	359	53.3	121	2	H37266 Ig heavy chain V r
80	358.5	53.2	147	2	PH1561 Ig heavy chain V r
81	357	53.0	98	2	PH0871 Ig heavy chain V r
82	357	53.0	118	2	S38565 Ig heavy chain V r
83	357	53.0	140	2	PH1482 Ig heavy chain V r
84	356.5	52.9	117	2	B27563 Ig heavy chain V r
85	356	52.8	119	2	PH0899 Ig heavy chain V r
86	356	52.8	121	2	F37266 Ig heavy chain V r
87	355	52.7	111	2	PH0993 Ig heavy chain V r
88	355	52.7	113	2	PH1663 Ig heavy chain V r
89	355	52.7	125	2	S20639 Ig heavy chain V r
90	355	52.7	142	2	S19245 Ig heavy chain pre
91	354.5	52.6	119	2	F49590 Ig heavy chain V r
92	354	52.5	111	2	PH0932 Ig heavy chain V r
93	353	52.4	117	2	PH0932 Ig heavy chain V r
94	353	52.4	140	2	T01407 Ig heavy chain (my
95	352.5	52.3	119	2	JN0295 Ig heavy chain V-D
96	352.5	52.3	134	2	PH1422 Ig heavy chain V r
97	352	52.2	120	2	S03471 Ig heavy chain V-D
98	351.5	52.2	115	2	A54378 Ig heavy chain V r
99	351.5	52.2	120	2	S26789 Ig heavy chain V r
100	351	52.1	117	1	HVHU35 Ig heavy chain pre

ALIGNMENTS

RESULT 1

S36260
 IG heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
 C:Accession: S36260
 R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; McCafferty, J.
 EMBL J. 12, 725-734, 1993
 A:Title: Human anti-self antibodies with high specificity from phage display libraries.
 A:Reference number: S36256; MUID:93178448; PMID:7679990
 A:Accession: S36260
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-129 <GI>
 A:Cross-references: EMBL:Z18851; NID:G33124; PTDN:CAA79303.1; PID:g939903
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IM>

```

Query Match      67.2%; Score 453; DB 2; Length 129;
Best Local Similarity 70.6%; Pred. No. 6.8e-36;
Matches 89; Conservative 9; Mismatches 26; Indels 2; Gaps 1;

QY      1 LEQGAEEYKPGASVKYSCQASGVYRFSNFIHVHVRQAPGQRFEEWGWINFYNGNKEPSAK 60
      :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db       4 LQQGAEEYKPGASVKYSCKASGTFYTSYGISWVRQAPCGGLEWGWISAYNGNTNYAQK 63
      :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 FQDRYTFYFADTSANTAYMELRSLSADTAYYYCAR--VGPFYSWDDSPQDNYTYMDVWGKGT 118
      :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      64 LQGRVTMTDTSTSTAYMELRSLSDDTAYYYCARDSPGYCSSTCPYYYYYMDVWGKGT 123
      :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      119 TVIVSS 124
      :|:|||||
Db      124 TVTVSS 129
      :|:|||||

```

RESULT 2

R430001 2
 Ig heavy chain V region - human
 S46393
 C:Species: Homo sapiens (man)
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S46393
 R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
 J. Mol. Biol. 239, 53-78, 1994
 A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
 A:Reference number: S46390; MUID:94254092; PMID:8196048
 A:Accession: S46393
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-129 <FIG>
 A:Cross-references: EMBL:Z31680; NID:g508786; PIDN:CAA83485.1; PID:g1335146
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-9a/Domain: immunoglobulin homology <IMM>

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Query Match          56.6%; Score 449; DB 2; Length 129;
Best Local Similarity 59.0%; Pred. No. 1.6e-35;
Matches 87; Conservative 9; Mismatches 28; Indels 2; Gaps 1

QY      1 LEQSAEYKKPGASVKYSQASGYRFSFNVIHVRQAPGQRFEMWGWINPYNNGNKEFSAK 60
DB      4 LVQSAEYKKPGASVKYSCKASGYTFGTGYHWHVRQAPGGGLEWGWINPNSGGTNYAQK 63

QY      61 FQDRYTFADTASANTAYNELSLRSADTAVYICARVGYPYSWDDSP--QNYTMDYVWGKT 118
DB      64 FQGWTTMTDTSISTAYWELSLRSDTAVYICARQSAVYDSSGYYSANTYMDYVWGKT 123

QY      119 TVIVSS 124
DB      124 TVTVSS 129

```

RESULT 3

PH1666
 Ig heavy chain V region (clone 6C9) - human (fragment)
 C-Species: Homo sapiens (man)
 C-Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C-Accession: PH1666
 R-Hillison, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Sasso, E.H.
 J. Exp. Med. 178, 331-336, 1993
 A-Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococci
 A-Reference number: PH1642; MUID:93301610; PMID:8315388
 A-Accession: PH1666
 A-Molecule type: mRNA
 A-Residues: 1-118 <HIL>
 A-Experimental source: B cell
 C-Superfamily: immunoglobulin V region; immunoglobulin homology
 C-Keywords: heterotetramer; immunoglobulin
 F:7-90/Domain: immunoglobulin homology <IMM>

Query Match	64.3%;	Score	433.5;	DB	2;	Length	118;
Best Local Similarity	70.2%;	Pred. No.	4.3e-34;				
Matches	85;	Conservative	12;	Mismatches	19;	Indels	5; Gaps 2
QY	6	AEVKKPGASVKVSCQASGYSRFSNFIHVTWVQAQGRFEMWGMINPVGNGKFSAXFQQRV	65				
DB	1	AEVKKPGASVKVSCKASGYTFTSYAHVHWVQAQGRLEWNGWINAGNGNTKYAQHFGQQRV	60				
QY	66	TFTADTASNTAYMELSLRSGADTAVYYCARVGPYSWDDSPQDNY--MDVWGKGTTTVIS	123				
DB	61	TIITDTSASITAYMELSLRSGDADTAVYYCARV---TLDGGIKFIYYGYGMDVWGQTTTVIS	117				
QY	124	S	124				
DB	118	S	118				

RESULT 4

19665
 Ig heavy chain V region (alpha-phOx15) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
 C:Accession: S19665; S24442
 R:Marks, J.D.; Hooenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 591-597, 1991
 A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage particles.
 A:Reference number: S19663; MUID:92085276; PMID:1748994
 A:Accession: S19665
 A:Molecule type: mRNA
 A:Residues: 1-124 <MAP>
 A:Cross-references: EMBL:X61647
 R:Jones, P.T.
 submitted to the EMBL Data Library, October 1991
 A:Reference number: S24442
 A:Accession: S24442
 A:Molecule type: mRNA
 A:Residues: 1-40, 'GISGWDGSAITWTQSIIDK', 61-118, 'T' 120-124 <JON>
 A:Cross-references: EMBL:X61647; NID:G57667; PID:CAA43828.1; PID:G1335368
 A:Note: the difference for residues 41-60 results from misplacement of 10 bases in the s.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/main: immunoglobulin homology <IMM>

```

Query Match      64.2%; Score 432.5; DB 2; Length 124;
Best Local Similarity 67.7%; Pred. No. 5,7e-34;
Matches 84; Conservative 13; Mismatches 24; Indels 3; Gaps 1
QY      1 LEQGAEVKPGASVKVSCAAGYRFSNFVIHWVRQAPGQRFEMWGWINPYNGNKEFSAK 60
Db       4 LVQGAEVKPGASVKVSCAKSGYTTISYICISWVRQAPQGLEWGWISAYNGNTKYAQK 63
QY      61 FQDRVTFADTSANTAYMEILRSADTAVYCARVGPVSWDSDPDNYYMDVWGKGVTV 120

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Db 64 LQGRVTMTDTSTSTAYMELSLRSDDTAVYVCVRLLP---KRTATLHYIYDVMGKGTIV 120
QY 121 IVSS 124
    |||
Db 121 TVSS 124

RESULT 5
IG heavy chain V region (clone 2H7) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1667
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1667
A:Molecule type: mRNA
A:Residues: 1-114 <HIL>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 62.8%; Score 423.5; DB 2; Length 114;
Best Local Similarity 68.3%; Pred. No. 3.7e-33;
Matches 82; Conservative 12; Mismatches 19; Indels 7; Gaps 3;

QY 6 AEVKKPGASVKVSCQASGYRFSNFVTHWVRQAPGQRFPEWGMINPYNGNKEFSAK 65
Db 1 AEVKKPGASVKVSCASGYTFTSYAHWVRQAPGQSLWGMINAGNGNTKYAQKPGSRV 60

QY 66 TFTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYI-MDVWGKGTIVVSS 124
Db 61 TITRDTASATAYMELSLRSSEDTAVYVCARVYDF-W-----SGYAFDIWGQGTMTVSS 114

RESULT 6
S29257
IG heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S29257
R:Chouhane, L.; van Spronsen, A.; Breyer, J.; Guglielmi, P.; Strosberg, A.D.
Eur. J. Biochem. 207, 1115-1121, 1992
A:Title: Molecular characterization of a human anti-Bh(D) antibody with a D(H) segment
A:Reference number: S29257; MUID:92382614; PMID:1499555
A:Accession: S29257
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <CHO>
A:Cross-references: GB:S42403; NID:9253699; PIDN:AAB22940.1; PID:9253700
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.2%; Score 419; DB 2; Length 148;
Best Local Similarity 62.7%; Pred. No. 1.3e-32;
Matches 84; Conservative 11; Mismatches 21; Indels 18; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVTHWVRQAPGQRFPEWGMINPYNGNKEFSAK 60
Db 23 LVQSGAEVKKPGASVKVSCASGYTFTAYAHWVRQAPGQSLWGMISVADGKTKYSQK 82

QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNY-----Y 110
Db 83 FQDRVTITRDTSATAYMEVRLSRSEDTAVYVCAR-----SPRINNVRLVITTPW 134

QY 111 MDVWGKGTIVVSS 124
    |||
Db 135 FDSWGQGTIVVSS 148
```

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RESULT 7
D33548
IG heavy chain V-1 region (WIL2) - human
C:Species: Homo sapiens (man)
C>Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D33548
R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression in B cell precursors
A:Reference number: A33548; MUID:89345575; PMID:2503826
A:Accession: D33548
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-123 <KIP>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 61.9%; Score 417; DB 2; Length 123;
Best Local Similarity 65.3%; Pred. No. 1.7e-32;
Matches 81; Conservative 9; Mismatches 30; Indels 4; Gaps 1;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVTHWVRQAPGQRFPEWGMINPYNGNKEFSAK 60
Db 4 LVQSGAEVKKPGASVKVSCASGYTFTGHYMHVVRQAPGQGLEWGMINPNSGGTNYAEK 63

QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYIYDVWGKGTIV 120
Db 64 FQGRVTITRDTSTINTAYMELSLRSDDTAVYVCARASYCYGD----CYFFFDYWGQGTIV 119

QY 121 IVSS 124
    |||
Db 120 TVSS 123

RESULT 8
S36265
IG heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36265
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36265
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-118 <GRI>
A:Cross-references: EMBL:Z18846; NID:933121; PIDN:CAA79298.1; PID:9939900
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 416.5; DB 2; Length 118;
Best Local Similarity 65.1%; Pred. No. 1.8e-32;
Matches 82; Conservative 11; Mismatches 20; Indels 13; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVTHWVRQAPGQRFPEWGMINPYNGNKEFSAK 60
Db 4 LVQSGAEVKKPGASVKVSCASGYTFTGYNHVVRQAPGQGLEWGMINPNSGGTNYAQK 63

QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQD---NTYMDVWGKGT 118
Db 64 FQGRVTITRDTSTAYMELSLRSSEDTAVYVCAR-----DPLSGYLDYWGQGT 112

QY 119 TVIVSS 124
    |||
Db 113 LTVSS 118

RESULT 9
C33548
```

Ig heavy chain V-1 region (783) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: C33548
R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression
A:Reference number: A33548; MUID:89345575; PMID:2503826
A:Accession: C33548
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1-133 <KIP>
A:Experimental source: the sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IM>
Query Match 61.3%; Score 413; DB 2; Length 133;
Best Local Similarity 65.4%; Pred. No. 4.3e-32; Indels 2;
Matches 85; Conservative 11; Mismatches 28; Gaps 6; Gaps 2;
Qy 1 LEQSGAEVKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWINPYNGNKEFSK 60
Db 4 LVQSGAEVKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWIIPIFGTANYAQK 63
Qy 61 FQGRVTFTADTSANTAYMELRSADTAVYCAR---VGPYSWDDSPQDNY---MDVW 114
Db 64 FQGRVTITADESTAYMELSLRSEDVAVYCAKTIIGLPYSSGWPNSDYYVGMVW 123
Qy 115 GKGTITVSS 124
Db 124 QGTTITVSS 133
RESULT 10
S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
A:Reference number: S14683; MUID:90332450; PMID:2115996
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-627 <FRI>
A:Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin; membrane protein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-627/Product: Ig mu chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IM>
Query Match 61.3%; Score 413; DB 2; Length 627;
Best Local Similarity 65.4%; Pred. No. 2.2e-31; Indels 6; Gaps 2;
Matches 85; Conservative 11; Mismatches 28; Indels 6; Gaps 2;
Qy 1 LEQSGAEVKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWINPYNGNKEFSK 60
Db 23 LVQSGAEVKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWIIPIFGTANYAQK 82
Qy 61 FQGRVTFTADTSANTAYMELRSADTAVYCAR---VGPYSWDDSPQDNY---MDVW 114
Db 83 FQGRVTITADESTAYMELSLRSEDVAVYCAKTIIGLPYSSGWPNSDYYVGMVW 142
Qy 115 GKGTITVSS 124
Db 143 QGTTITVSS 152
RESULT 11
PH0955

Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0955
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1152291
A:Accession: PH0955
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-127 <MAZ>
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-115/Region: complementarity-determining 3
Query Match 60.5%; Score 408; DB 2; Length 127;
Best Local Similarity 66.9%; Pred. No. 1.2e-31; Indels 0; Gaps 0;
Matches 83; Conservative 8; Mismatches 33; Indels 0; Gaps 0;
Qy 1 LEQSGAEVKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWINPYNGNKEFSK 60
Db 4 LVQSGAEVKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWIIPIFGTANYAQK 63
Qy 61 FQGRVTFTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWKGTTV 120
Db 64 FQGRVTITADESTAYMELSLRSEDVAVYCARVIFGVVQHYVYMDVWKGTTV 123
Qy 121 IVSS 124
Db 124 TVSS 127
RESULT 12
S31600
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31600
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CUI>
A:Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IM>
Query Match 59.7%; Score 402.5; DB 2; Length 136;
Best Local Similarity 63.7%; Pred. No. 4.3e-31; Indels 11; Gaps 2;
Matches 79; Conservative 14; Mismatches 20; Indels 11; Gaps 2;
Qy 1 LEQSGAEVKPGASVKVSCQASGYRFSNFVHWVRAQPGQRFEMWGWINPYNGNKEFSK 60
Db 23 LVQSGAEVKPGASVKVSCASGYTFTSYDINWVRAQPGQRFEMWGWINPYNGNKEFSK 82
Qy 61 FQGRVTFTADTSANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWKGTTV 120
Db 83 FQGRVTITADESTAYMELSLRSEDVAVYCAR-----WRDA-----FDIWGQGTIV 131
Qy 121 IVSS 124
Db 132 TVSS 135

RESULT 13

ELHUND
Ig heavy chain precursor V-I region (Nd) - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000
C:Accession: A93933; A02026
R:Kenter, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A:Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon
A:Reference number: A93933; MUID:93065234; PMID:6815656
A:Accession: A93933
A:Molecule type: mRNA
A:Residues: 1-143 <XEN>
R:Bannich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
A:Reference number: A94418
A:Contents: annotation; partial sequence
A:Note: this epsilon chain was isolated from a myeloma protein
C:Genetics:
A:Gene: GDB:IGHV@
A:Cross-references: GDB:128528; OMIM:147070
A:Map Position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-143/Product: Ig heavy chain V-I region (Nd) #status predicted <MAT>
F:30-113/Domain: immunoglobulin homology <IMM>
F:16/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F:37-111/Disulfide bonds: #status experimental

Query Match 59.7%; Score 402.5; DB 1; Length 143;
Best Local Similarity 60.3%; Pred. No. 4.6e-31;
Matches 76; Conservative 20; Mismatches 27; Indels 3; Gaps 2;
QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 60
DB 19 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 60
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVPYSWDD--SPQDNYMDVWGKCT 118
DB 79 FQGRVTITADSTSTAYMELSLRSDDSAVFYCAKSDPP-WSDDYNYFDYSYILDVWGQGT 137
QY 119 TTVVSS 124
DB 138 TTVVSS 143

RESULT 14

S38271
Ig heavy chain V region (clone alpha-THY-29) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36271
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-122 <GRI>
A:Cross-references: EMBL:Z18832; NID:g33115; PIDN:CAA79284.1; PID:g939895
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 59.3%; Score 400; DB 2; Length 122;
Best Local Similarity 63.7%; Pred. No. 6.6e-31;
Matches 79; Conservative 11; Mismatches 24; Indels 10; Gaps 3;
QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 60

DB 4 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVPYSWDDSPQDNYMDVWGK 116
DB 64 LQGRVTITADSTSTAYMELSLRSDDSAVFYCAADTRIDDF-W-----SGYNFDYWGQ 117
QY 117 GTTV 120
DB 118 GTIV 121

RESULT 15

S46394
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46394
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46394
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <FIG>
A:Cross-references: EMBL:Z31681; NID:g509788; PIDN:CAA83486.1; PID:g1335147
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 59.1%; Score 398.5; DB 2; Length 132;
Best Local Similarity 64.1%; Pred. No. 1e-30;
Matches 84; Conservative 6; Mismatches 32; Indels 9; Gaps 2;
QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSK 60
DB 4 LVQSGAEVKKPGSSVKVSCKASGGTSSYALSWVRQAPGQGLEWGGIIPFGTANHAQK 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCAR-----VGPYSWDDSPQDNYMDV 113
DB 64 FQGRVTITADSTSTAYMELSLRSDDSAVFYCAADTGILEW--LPSYYNYMDV 121
QY 114 WGKGTITVSS 124
DB 122 WGKGTITVSS 132

RESULT 16

S18553
Ig heavy chain V region precursor (VI-3b) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18553; S26916
R:Shin, E.K.; Matsuda, F.; Nagakura, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Hc
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18553
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62109
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of v
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26916
A:Molecule type: DNA
A:Residues: 20-117 <TOM>
A:Cross-references: EMBL:Z12327; NID:g32871; PIDN:CAA78197.1; PID:g32872
C:Genetics:
A:Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-117/Product: Ig heavy chain V region (VI-3b) #status predicted <MAT>
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 397; DB 2; Length 117;
 Best Local Similarity 77.9%; Pred. No. 1.2e-30;
 Matches 74; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 LEOSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNNGKEFSK 60
 DB 23 LVQSGAEVKPGASVKVSCASGTFSSYAIISWRQAPGQGLEWGGIIPFGTANYAQK 82
 QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYICAR 95
 DB 83 FQGRVTITRTSASTAYMELSLRSEDVAVYICAR 117

RESULT 17
 S34014
 Ig heavy chain V region - human
 C;Species: Homo sapiens (man)
 C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
 C;Accession: S34014; S30535
 R;Martielle, X.; Tsapis, A.; Brouet, J.C.
 Eur. J. Immunol. 23, 846-851, 1993
 A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
 A;Reference number: S34001; MUID:93209281; PMID:7681398
 A;Accession: S34014
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-127 <VAR>
 A;Cross-references: EMBL:Z18321
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 58.8%; Score 396; DB 2; Length 127;
 Best Local Similarity 60.3%; Pred. No. 1.7e-30;
 Matches 79; Conservative 15; Mismatches 19; Indels 18; Gaps 2;

QY 3 QSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNNGKEFSK 62
 DB 6 QSGAEVKKPGASVKVSCASGYFTSYDINWRQATCGGLEWGWNPSSGNTGYAKFK 65
 QY 63 DRVTFADTSANTAYMELSLRSADTAVYICARV-----GPSWDDSPQNTYMDV 113
 DB 66 GRVTMTNTSTAYMELSLRSEDVAVYICARALSIGAVIRGY-----YALDV 116

QY 114 WKGTTTVSS 124
 DB 117 WQGGTTTVSS 127

RESULT 18
 B33548
 Ig heavy chain V-1 region (AND) - human
 C;Species: Homo sapiens (man)
 C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
 R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
 A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene exp
 A;Reference number: A33548; MUID:89345575; PMID:2503826
 A;Accession: B33548
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A;Molecule type: DNA
 A;Residues: 1-126 <KIP>
 A;Experimental source: the sequence was determined from the differentiated gene
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 58.7%; Score 395.5; DB 2; Length 126;
 Best Local Similarity 63.8%; Pred. No. 1.8e-30;
 Matches 83; Conservative 8; Mismatches 26; Indels 13; Gaps 2;

QY 1 LEOSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNNGKEFSK 60
 DB 4 LVQSGAEVKKPGASVKVSCASGTFSSYAIISWRQAPGQGLEWGGIIPFGTANYAQK 63
 QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYICARV-----PYSWDDSPQNTYMDV 114
 DB 64 FQGRVTITADESTAYMELSLRSEDVAVYICARVIFGVQHYHY-----YYMDV 116

QY 115 GKGTTTVSS 124
 DB 117 GLGTTTVSS 126

RESULT 19

PH0954
 Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C;Accession: PH0954
 R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A;Title: Evidence for somatic selection of natural autoantibodies.
 A;Reference number: PH0952; MUID:92202880; PMID:1552291
 A;Accession: PH0954
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-132 <MAR>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-30/Region: framework 1
 F;15-98/Domain: immunoglobulin homology <IMM>
 F;31-35/Region: complementarity-determining 1
 F;36-50/Region: framework 2
 F;51-67/Region: complementarity-determining 2
 F;68-98/Region: framework 3
 F;99-120/Region: complementarity-determining 3

Query Match 58.7%; Score 395.5; DB 2; Length 132;
 Best Local Similarity 63.4%; Pred. No. 1.9e-30;
 Matches 83; Conservative 10; Mismatches 29; Indels 9; Gaps 2;

QY 1 LEOSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFWMGWINPYNNGKEFSK 60
 DB 4 LVQSGAEVKKPGSSVKVSCASGTFSSYAIISWRQAPGQGLEWGGIIPFGTANYAQK 63
 QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYICARVGPSWDDSPQNTY-----MDV 113
 DB 64 FQGRVTITADESTAYMELSLRSEDVAVYICAR--PHASIDDFWSGYPNYYYGMDV 121

QY 114 WKGTTTVSS 124
 DB 122 WQGGTTTVSS 132

RESULT 20

S49530
 anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
 C;Species: Homo sapiens (man)
 C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
 C;Accession: S49530
 R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 submitted to the EMBL Data Library, October 1994
 A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
 A;Reference number: S48797
 A;Accession: S49530
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-135 <MAH>

A;Cross-references: EMBL:Z46348; NID:G560839; PIDN:CRA86467.1; PID:G560840
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.7%; Score 395.5; DB 2; Length 135;
Best Local Similarity 62.9%; Pred. No. 2e-30;
Matches 78; Conservative 11; Mismatches 24; Indels 11; Gaps 2;
QY 1 LEQSGAEVKKPGASVKVSQASGVRFSNFVTHWVROAPGQRFEMWGNINPYNKKEFSK 60
DB 23 LVQSGAEVKKPGASVKVSQASGVRFSNFVTHWVROAPGQRFEMWGNINPYNKKEFSK 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWKGTTV 120
DB 83 FQGRVTMTDTSISTAYMELSLRLSDTAVYYCARA-----RTGY--NHWGQGTIV 131
QY 121 IVSS 124
DB 132 TVSS 135

RESULT 21

A49590
Ig heavy chain V region (ACHSV1, clone 15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-May-1997
C;Accession: A49590
R;Burioni, R.; Williamson, R.A.; Sanna, P.P.; Bloom, F.E.; Burton, D.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 355-359, 1994
A;Title: Recombinant human Fab to glycoprotein D neutralizes infectivity and prevents cell fusion
A;Reference number: A49590; MUID:94105186; PMID:8278393
A;Accession: A49590
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-121 <BUR>
A;Experimental source: bone marrow lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIP:141850)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;11-94/Domain: immunoglobulin homology <IMM>

Query Match 58.5%; Score 394; DB 2; Length 121;
Best Local Similarity 66.4%; Pred. No. 2.4e-30;
Matches 81; Conservative 10; Mismatches 29; Indels 2; Gaps 1;
QY 3 QSGAEVKKPGASVKVSQASGVRFSNFVTHWVROAPGQRFEMWGNINPYNKKEFSK 62
DB 2 ESGAEVKKPGSSVKVSCKTSGGAFSSYAINWVROAPGQGLEWNGGILPVFGTTNEA 61
QY 63 DRYTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWKGTTV 122
DB 62 GRVTFADASTAYMELSLRLSDTAVYCARVGVCSYNGCSLGG--MDVWGQGTIV 119
QY 123 SS 124
DB 120 SS 121

RESULT 22

S23623
Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S23623
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from B6 mice
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23623
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-171 <OLE>
A;Cross-references: EMBL:X59702; NID:G32010; PIDN:CAA42223.1; PID:G32011

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.4%; Score 393.5; DB 2; Length 171;
Best Local Similarity 63.0%; Pred. No. 3.9e-30;
Matches 80; Conservative 11; Mismatches 29; Indels 7; Gaps 3;
QY 1 LEQSGAEVKKPGASVKVSQASGVRFSNFVTHWVROAPGQRFEMWGNINPYNKKEFSK 60
DB 23 LVQSGAEVKKPGASVKVSQASGVRFSNFVTHWVROAPGQRFEMWGNINPYNKKEFSK 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWKGTTV 117
DB 83 FQGRVTMTDTSISTAYMELSLRLSDTAVYYCAI--EYFDGSLKPSDVF--DINGQG 138
QY 118 TTVIVSS 124
DB 139 TMTVTSS 145

RESULT 23

PH1665
Ig heavy chain V region (clone 6B8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1665
R;Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1665
A;Molecule type: mRNA
A;Residues: 1-104 <HIL>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 58.2%; Score 392.5; DB 2; Length 104;
Best Local Similarity 64.7%; Pred. No. 2.9e-30;
Matches 77; Conservative 10; Mismatches 17; Indels 15; Gaps 1;
QY 6 AEVKKPGASVKVSQASGVRFSNFVTHWVROAPGQRFEMWGNINPYNKKEFSK 65
DB 1 AEVKKPGASVKVSQASGVRFSNFVTHWVROAPGQRFEMWGNINPYNKKEFSK 60
QY 66 TFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWKGTTV 124
DB 61 TITRDTASTAYMELSLRLSDTAVYYCAR-----EDYWGQGTIVTSS 104

RESULT 24

PH0961
Ig heavy chain V region (G6+ T-133) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0961
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0961
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-119 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;11-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2

F:15-98/Region: framework 3
F:99-107/Region: complementarity-determining 3

Query Match 58.2%; Score 392; DB 2; Length 119;
Best Local Similarity 66.1%; Pred. No. 3.7e-30;
Matches 82; Conservative 9; Mismatches 25; Indels 8; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFVHVRQAPGQRFWMGWINPYNGNKFSK 60
DB 4 LVQSGAEVKPGASVKVSCQASGYRFSNFVHVRQAPGQRFWMGWINPYNGNKFSK 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 64 FQGRVTITADESTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 115
QY 121 IVSS 124
DB 116 TVSS 119

RESULT 25
S31999
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999
C:Accession: S31999
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A:Reference number: S31977
A:Accession: S31999
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <MOR>
A:Cross-references: EMBL:Z45084; NID:G38507; PIDN:CAA78793.1; PID:G38508
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 390.5; DB 2; Length 120;
Best Local Similarity 60.0%; Pred. No. 5.2e-30;
Matches 75; Conservative 16; Mismatches 25; Indels 9; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFVHVRQAPGQRFWMGWINPYNGNKFSK 60
DB 4 LLESGAEVKPGASVKVSCQASGYRFSNFVHVRQAPGQRFWMGWINPYNGNKFSK 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTT 119
DB 64 FQGRVTITADESTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTT 115
QY 120 IVSS 124
DB 116 TVSS 120

RESULT 26
S26792
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26792
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami
A:Reference number: S26786; MUID:92111632; PMID:11730251
A:Accession: S26792
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <MOR>
A:Cross-references: EMBL:X61012; NID:G32804; PIDN:CAA43346.1; PID:G1335131
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 390; DB 2; Length 131;
Best Local Similarity 59.4%; Pred. No. 6.3e-30;
Matches 76; Conservative 18; Mismatches 30; Indels 4; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFVHVRQAPGQRFWMGWINPYNGNKFSK 60
DB 4 LVQSGAEVKPGASVKVSCQASGYRFSNFVHVRQAPGQRFWMGWINPYNGNKFSK 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGK 116
DB 64 FTGRFVSLDTSVTAQLQSSLKAEATVYCARVGPYSWDDSPQDNYMDVWGK 123
QY 117 GTTVIVSS 124
DB 124 GTTVIVSS 131

RESULT 27
PH0958
Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0958
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0958
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-122 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-110/Region: complementarity-determining 3

Query Match 57.8%; Score 389.5; DB 2; Length 122;
Best Local Similarity 63.8%; Pred. No. 6.5e-30;
Matches 81; Conservative 10; Mismatches 25; Indels 11; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFVHVRQAPGQRFWMGWINPYNGNKFSK 60
DB 4 LVQSGAEVKPGASVKVSCQASGYRFSNFVHVRQAPGQRFWMGWINPYNGNKFSK 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGK 117
DB 64 FQGRVTITADESTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGK 115
QY 118 TTVIVSS 124
DB 116 TTVIVSS 122

RESULT 28
PH0952
Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0952
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0952
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA

A;Residues: 1-128 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-116/Region: complementarity-determining 3

Query Match 57.8%; Score 389.5; DB 2; Length 128;
Best Local Similarity 64.3%; Pred. No. 6.9e-30;
Matches 81; Conservative 10; Mismatches 32; Indels 3; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMMGWINPYNGNKEFSAK 60
DB 4 LVQSGAEVKPGSVKVCASGGTFSYAIWVRQAPGQGLEWVGIIPIFTANYAQK 63

QY 61 FQDRVTFTADTSANTAYMELRSADTAVYCARVGPYS--WDDSPQDNYMDVWGKGT 118
DB 64 FQGRVTITADKSTSTAYMELSLRSEDATVYVCARGGNVDYIW-GSYRSNDAPDIWGQST 122

QY 119 TVIVSS 124
DB 123 MVTVSS 128

RESULT 29
B32274
Ig heavy chain precursor V-I region (EVI-15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Oct-1996
C;Accession: B32274
R;Newkirk, M.M.; Gram, H.; Heinrich, G.F.; Oestberg, L.; Capra, J.D.; Wasserman, R.L.
J. Clin. Invest. 81, 1511-1518, 1988
A;Title: Complete protein sequences of the variable regions of the cloned heavy and light actors of the Wa idiotype family
A;Reference number: A92767; MUID:88213701; PMID:2452836
A;Accession: B32274
A;Molecule type: DNA
A;Residues: 1-135 <NEW>
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;4-135/Product: Ig heavy chain V-I region EVI-15 #status predicted <HVI>
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 57.3%; Score 386.5; DB 2; Length 135;
Best Local Similarity 60.7%; Pred. No. 1.4e-29;
Matches 82; Conservative 10; Mismatches 26; Indels 17; Gaps 4;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMMGWINPYNGNKEFSAK 60
DB 7 LVQSGAEVKPGSVKVCASGGTFSYAFWVRQAPGQGLEWVGIIPIFLGTHYQAK 66

QY 61 FQDRVTFTADTSANTAYMELRSADTAVYCARVGPYSWDDSDS-----POD-NY-- 110
DB 67 FQDRVIITDBSTRTAYMELHILRSEDATVYCAR-----DOSLENIEVPLDPNIFYD 120

QY 111 -MDVWGKGTIVVSS 124
DB 121 GMDVWGQGTIVTVSS 135

RESULT 30
A32483
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C;Accession: A32483
R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, O

Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells using A:Reference number: A32483; MUID:89273586; PMID:2499327
A;Accession: A32483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-142 <LAR>
A;Cross-references: GB:M26463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>

Query Match 57.3%; Score 386; DB 2; Length 142;
Best Local Similarity 57.7%; Pred. No. 1.6e-29;
Matches 79; Conservative 9; Mismatches 23; Indels 26; Gaps 2;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMMGWINPYNGNKEFSAK 60
DB 14 LVQSGAEVKPGASVKVSCASGTYFTINYHWVRQAPGQGLEWVGIIIPSGNSTNYAQK 73

QY 61 FQDRVTFTADTSANTAYMELRSADTAVYCAR-----VGPSWDDSDSQD 107
DB 74 FQGRVTMTDRDTSSTVYMELSLRSEDATVYVCAREKLATTFGVLIITG----- 123

QY 108 NYMDVWGKGTIVVSS 124
DB 124 ---MDYWGQGTIVTVSS 137

Search completed: August 26, 2004, 13:39:51
Job time : 13.9407 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:33:27 ; Search time 7.34815 Seconds
(without alignments)
878.684 Million cell updates/sec

Title: US-10-016-986-66

Perfect score: 674

Sequence: 1 LEQSGAEVKKPGASVKVSQ.....PQDNYMDYMGKGTIVVSS 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	402.5	59.7	147	1	HVIC HUMAN
2	363.5	53.9	120	1	HV1H HUMAN
3	361	53.6	117	1	HV1E HUMAN
4	357	53.0	120	1	HV03 MOUSE
5	353	52.4	117	1	HV12 MOUSE
6	351	52.1	117	1	HV1G HUMAN
7	348	51.6	117	1	HV13 MOUSE
8	344.5	51.1	118	1	HV51 MOUSE
9	342.5	50.8	139	1	HV07 MOUSE
10	339.5	50.4	120	1	HV50 MOUSE
11	339.9	50.3	140	1	HV02 MOUSE
12	325.5	48.3	137	1	HV11 MOUSE
13	324	48.1	138	1	HV48 MOUSE
14	321.5	47.7	114	1	HV00 MOUSE
15	321	47.6	117	1	HV1A HUMAN
16	319	47.3	125	1	HV1F HUMAN
17	318	47.2	121	1	HV01 MOUSE
18	315	46.7	117	1	HV14 MOUSE
19	310	46.0	136	1	HV15 MOUSE
20	309	45.8	117	1	HV09 MOUSE
21	307	45.5	117	1	HV04 MOUSE
22	303	45.0	117	1	HV52 MOUSE
23	300.5	44.6	119	1	HV38 MOUSE
24	297	44.1	117	1	HV06 MOUSE
25	292	43.3	117	1	HV49 MOUSE
26	287	42.6	117	1	HV10 MOUSE
27	286	42.4	117	1	HV05 MOUSE
28	285.5	42.4	136	1	HV16 MOUSE
29	279.5	41.5	122	1	HV3G HUMAN
30	278.5	41.3	124	1	HV1E HUMAN
31	276.5	41.0	122	1	HV20 MOUSE
32	276	40.9	123	1	HV25 MOUSE
33	275	40.8	121	1	HV3J HUMAN

ALIGNMENTS

RESULT 1

34	275	40.8	123	1	HV22 MOUSE	P01791 mus musculus
35	273.5	40.6	122	1	HV21 MOUSE	P01790 mus musculus
36	273.5	40.6	124	1	HVID HUMAN	P01760 homo sapien
37	272.5	40.4	122	1	HV3H HUMAN	P01769 homo sapien
38	272	40.4	118	1	HV39 MOUSE	P01809 mus musculus
39	272	40.4	119	1	HV3I HUMAN	P01770 homo sapien
40	272	40.4	123	1	HV19 MOUSE	P01788 mus musculus
41	271.5	40.3	119	1	HV37 MOUSE	P01807 mus musculus
42	271	40.2	123	1	HV18 MOUSE	P01787 mus musculus
43	270	40.1	123	1	HV23 MOUSE	P01792 mus musculus
44	270	40.1	123	1	HV24 MOUSE	P01793 mus musculus
45	268.5	39.8	119	1	HV40 MOUSE	P01810 mus musculus
46	266.5	39.5	146	1	HV2I HUMAN	P06331 homo sapien
47	265	38.3	117	1	HV42 MOUSE	P01812 mus musculus
48	264	38.2	144	1	HV26 MOUSE	P01795 mus musculus
49	261	38.7	117	1	HV4I MOUSE	P01811 mus musculus
50	260.5	38.6	119	1	HV3P HUMAN	P01777 homo sapien
51	260	38.6	115	1	HV3D HUMAN	P01765 homo sapien
52	256	38.0	137	1	HV46 MOUSE	P01822 mus musculus
53	255.5	37.9	126	1	HV3K HUMAN	P01772 homo sapien
54	253.5	37.6	122	1	HV3A HUMAN	P01762 homo sapien
55	250	37.1	144	1	HV43 MOUSE	P01819 mus musculus
56	249	36.9	142	1	HV0I RAT	P01805 rattus norv
57	243.5	36.1	116	1	HV3T HUMAN	P01781 homo sapien
58	242.5	36.0	120	1	HV3U HUMAN	P01782 homo sapien
59	242	35.9	120	1	HV3E HUMAN	P01766 homo sapien
60	241	35.8	119	1	HV3L HUMAN	P01773 homo sapien
61	240.5	35.7	115	1	HV3S HUMAN	P01780 homo sapien
62	240	35.6	116	1	HV36 MOUSE	P01806 mus musculus
63	240	35.6	117	1	HV2G HUMAN	P01825 homo sapien
64	239	35.5	116	1	HV3R HUMAN	P01779 homo sapien
65	238.5	35.4	117	1	HV3O HUMAN	P01776 homo sapien
66	238	35.3	115	1	HV3F HUMAN	P01767 homo sapien
67	237.5	35.2	111	1	HV35 MOUSE	P01804 mus musculus
68	237.5	35.2	118	1	HV3V HUMAN	P0419 homo sapien
69	237	35.2	129	1	HV2F HUMAN	P01824 homo sapien
70	236.5	35.1	114	1	HV3B HUMAN	P01763 homo sapien
71	236.5	35.1	119	1	HV3M HUMAN	P01774 homo sapien
72	236	35.0	117	1	HV3C HUMAN	P01764 homo sapien
73	235	34.9	117	1	HV55 MOUSE	P01826 mus musculus
74	234.5	34.8	119	1	HV3N HUMAN	P01775 homo sapien
75	234.5	34.8	135	1	HV02 XENIA	P20957 xenopus lae
76	232	34.8	116	1	HV6I MOUSE	P18532 mus musculus
77	231	34.3	116	1	HV3Q HUMAN	P01778 homo sapien
78	231	34.3	117	1	HV17 MOUSE	P01786 mus musculus
79	230.5	34.2	114	1	HV0I CANFA	P01784 canis famil
80	229	34.0	113	1	HV30 MOUSE	P01799 mus musculus
81	229	34.0	115	1	HV32 MOUSE	P01801 mus musculus
82	228	33.8	117	1	HV54 MOUSE	P18525 mus musculus
83	227	33.7	117	1	HV03 CARAU	P19180 carassius a
84	225	33.4	115	1	HV33 MOUSE	P01796 mus musculus
85	224	33.2	113	1	HV27 MOUSE	P01802 mus musculus
86	224	33.2	117	1	HV01 CAICR	P01813 caiman croc
87	223.5	33.2	97	1	HV56 MOUSE	P18527 mus musculus
88	223	33.1	98	1	HV57 MOUSE	P18528 mus musculus
89	223	33.1	113	1	HV3I MOUSE	P01800 mus musculus
90	222	32.9	113	1	HV28 MOUSE	P01797 mus musculus
91	222	32.9	117	1	HV02 CANFA	P01785 canis famil
92	219	32.5	113	1	HV34 MOUSE	P01803 mus musculus
93	219	32.5	116	1	HV60 MOUSE	P18531 mus musculus
94	217	32.2	117	1	HV03 CAICR	P03982 caiman croc
95	217	32.2	117	1	HV58 MOUSE	P18529 mus musculus
96	217	32.2	121	1	HV2E HUMAN	P01818 homo sapien
97	215	31.9	113	1	HV29 MOUSE	P01798 mus musculus
98	215	31.8	117	1	HV53 MOUSE	P18524 mus musculus
99	214.5	31.8	116	1	HV05 CARAU	P19181 carassius a
100	214.5	31.8	116	1	HV45 MOUSE	P01821 mus musculus

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HV1C HUMAN
ID HV1C_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=95255299; PubMed=7737190;
RX Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RA "Characterization of the two unique human anti-flavin monoclonal
RT immunoglobulins."
RL Eur. J. Biochem. 228:896-893(1995).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01772; 2FB4.
GO GO:0005576; C:extracellular; NAS.
GO GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT DISULFID 22 95 BY SIMILARITY.
FT NON_TER 120 120
FT SEQUENCE 120 AA; 13272 MW; F1307FD253A782F1 CRC64;
SQ
SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 59.7%; Score 402.5; DB 1; Length 147;
Best Local Similarity 60.3%; Pred. No. 2.8e-35;
Matches 76; Conservative 20; Mismatches 27; Indels 3; Gaps 2;

QY 1 LEQSGAEVKKPGASVKVSQCOAGYRFSNFIHWVRQAPGQRFEMWGHPYNGKKEFSK 60
Db 23 LVQSGAEVKKPGASVKVSQCOAGYRFSNFIHWVRQAPGQRFEMWGHPYNGKKEFSK 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDD--SPQDNYVDVWGKGT 118
Db 83 FQGRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDD--SPQDNYVDVWGKGT 141
QY 119 TVIVSS 124
Db 142 TVIVSS 147

RESULT 2
HV1H HUMAN
ID HV1H_HUMAN STANDARD; PRT; 120 AA.
AC P80421;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region DOT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=83144028; PubMed=6298778;
RX Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RA "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups."
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DE Ig heavy chain V-I region DOT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=95255299; PubMed=7737190;
RX Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RA "Characterization of the two unique human anti-flavin monoclonal
RT immunoglobulins."
RL Eur. J. Biochem. 228:896-893(1995).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01772; 2FB4.
GO GO:0005576; C:extracellular; NAS.
GO GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT DISULFID 22 95 BY SIMILARITY.
FT NON_TER 120 120
FT SEQUENCE 120 AA; 13272 MW; F1307FD253A782F1 CRC64;
SQ
SEQUENCE 120 AA; 13272 MW; F1307FD253A782F1 CRC64;

Query Match 53.9%; Score 363.5; DB 1; Length 120;
Best Local Similarity 61.3%; Pred. No. 2.8e-31;
Matches 76; Conservative 13; Mismatches 28; Indels 7; Gaps 3;

QY 1 LEQSGAEVKKPGASVKVSQCOAGYRFSNFIHWVRQAPGQRFEMWGHPYNGKKEFSK 60
Db 4 LVQSGAEVKKPGASVKVSQCOAGYRFSNFIHWVRQAPGQRFEMWGHPYNGKKEFSK 62
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYVDVWGKGT 120
Db 63 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYVDVWGKGT 116
QY 121 IVSS 124
Db 117 IVSS 120

RESULT 3
HV1B HUMAN
ID HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=83144028; PubMed=6298778;
RX Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RA "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups."
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC or send an email to license@isb-sib.ch).

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CC -----
DR EMBL; J00240; AAA52988.1; -.
DR PIR; A02024; HVHUGH.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT DOMAIN 20 >117 IG-LIKE.
FT NON TER 117
FT SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;
SQ
Query Match 53.6%; Score 361; DB 1; Length 117;
Best Local Similarity 71.6%; Pred. No. 4.9e-31;
Matches 68; Conservative 9; Mismatches 18; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKSCQASGYSRFSNFIHVRQAPGQRFQFWMGWINPYNGNKEFSK 60
DB 23 LVQSGAEVKKPGASVKSCASGYTFSNYHVRQAPGQGLEWVGILNPSGGSTSYAQK 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCAR 95
DB 83 FQGRVTMTDSTSTVMYELSLRSADTAVYYCAR 117
RESULT 4
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Geiter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; HydrIdoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON TER 120
FT SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
SQ
Query Match 53.0%; Score 357; DB 1; Length 120;
Best Local Similarity 53.2%; Pred. No. 1.3e-30;
Matches 66; Conservative 26; Mismatches 26; Indels 6; Gaps 1;
QY 1 LEQSGAEVKKPGASVKSCQASGYSRFSNFIHVRQAPGQRFQFWMGWINPYNGNKEFSK 60
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DB 3 LQSGAEIVRAGSSVKMSCKASGYTFTSYGINWVQRPGQGLEWIGYINPGNGYTKYNEK 62
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPVSWDDSPQDNYNDVWGKGTTV 120
DB 63 FKGKATLTVDKSSSTAYMQLSLTSSEDSAVYFCARSVYIG-----GSYFDYWGCGTTL 116
QY 121 IVSS 124
DB 117 TVSS 120
RESULT 5
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC -!- SIMILARITY: THIS PROTEIN BINDS DEXTRAN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02039; MHMS4E.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (COMPLEX).
FT NON TER 117
FT SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
SQ
Query Match 52.4%; Score 353; DB 1; Length 117;
Best Local Similarity 54.0%; Pred. No. 3.4e-30;
Matches 67; Conservative 20; Mismatches 27; Indels 10; Gaps 2;
QY 1 LEQSGAEVKKPGASVKVSCQASGYSRFSNFIHVRQAPGQRFQFWMGWINPYNGNKEFSK 60
DB 4 LQSGPELVKPGASVKMSCKASGYTFTDYMKVKQSHGKSLWIGDINPNNGGTSYNQK 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPVSWDDSPQDNYNDVWGKGTTV 120
DB 64 FKGKATLTVDKSSSTAYMQLNSLTSEDSAVYFCAR--DYDW-----YFDVWGAGTTV 113
QY 121 IVSS 124
DB 114 TVSS 117
RESULT 6
HV1G_HUMAN
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno K., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus.";
RL EMOB J. 7:1047-1051(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVH35.
DR HSSP; P01772; 2PB4
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
KW CHAIN
FT SIGNAL 1 19 IG HEAVY CHAIN V-I REGION V35.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117
FT SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
SQ
Query Match 52.1%; Score 351; DB 1; Length 117;
Best Local Similarity 70.5%; Pred. No. 5.5e-30;
Matches 67; Conservative 8; Mismatches 20; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGNIPYNGKSFSAK 60
DB 23 LVQSGAEVKKPGASVKVSCASGYTFGTIHWVRQAPGQGLEWNGRINPNSGTYAQK 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCAR 95
DB 83 FQGRVTSTRTSISNTAYMELSLRSDDTVVYVCAR 117
RESULT 7
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J358.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";

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RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117
FT SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
SQ
Query Match 51.6%; Score 348; DB 1; Length 117;
Best Local Similarity 53.6%; Pred. No. 1.1e-29;
Matches 67; Conservative 20; Mismatches 26; Indels 12; Gaps 2;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGNIPYNGKSFSAK 60
DB 4 LQSGPELVKPGASVKVSKASGYTFITDYNMKWKQSHGKSLWIGDINPNNGTSTNQK 63
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNY-YMDVWGKGT 119
DB 64 FKGRATLVKSSSTAYMQLNSLTSSESAVYVCAR-----DRYWFVWGAGTT 112
QY 120 VIVSS 124
DB 113 VTVSS 117
RESULT 8
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMOB J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118
FT SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
SQ
Query Match 51.1%; Score 344.5; DB 1; Length 118;
Best Local Similarity 53.2%; Pred. No. 2.7e-29;
Matches 66; Conservative 21; Mismatches 28; Indels 9; Gaps 2;

```



```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sams J., Rabbits T.H., Estes P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1992).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00493; AAA38128.1; -.
CC PIR; A94264; HVMSG7.
CC HSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS0835; IG LIKE; 1.
CC Immunoglobulin V region; Hybridoma; Signal.
CC SIGNAL 1 19
CC CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
CC DOMAIN 20 139 IG-LIKE.
CC NON TER 140 140
CC SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 50.3%; Score 339; DB 1; Length 140;
Best Local Similarity 51.6%; Pred. No. 1.2e-28;
Matches 64; Conservative 25; Mismatches 29; Indels 6; Gaps 1;

QY 1 LEQSGAEVKPGASVKVSQASGYRFSNFIHVVRQAPGQRFWMGWINPYNKKEPSAK 60
Db 23 LQSGAEIVKPGASVKLSCKASGYTFTSYLHMVWVQPGGLEWIGIPNGYINYNEX 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYVMDVWGKTTV 120
Db 83 FRGKTLTVKSSSTAYMQLSLTSEDSAVYFCARSHYIG-----GSYDFDYWGQGTPL 136
QY 121 IVSS 124
Db 137 TVSS 140

RESULT 12
HV11 MOUSE
ID HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Keth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of

Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sams J., Rabbits T.H., Estes P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1992).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00493; AAA38128.1; -.
CC PIR; A94264; HVMSG7.
CC HSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS0835; IG LIKE; 1.
CC Immunoglobulin V region; Hybridoma; Signal.
CC SIGNAL 1 19
CC CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
CC DOMAIN 20 139 IG-LIKE.
CC NON TER 140 140
CC SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 50.3%; Score 339; DB 1; Length 140;
Best Local Similarity 51.6%; Pred. No. 1.2e-28;
Matches 64; Conservative 25; Mismatches 29; Indels 6; Gaps 1;

QY 1 LEQSGAEVKPGASVKVSQASGYRFSNFIHVVRQAPGQRFWMGWINPYNKKEPSAK 60
Db 23 LQSGAEIVKPGASVKLSCKASGYTFTSYLHMVWVQPGGLEWIGIPNGYINYNEX 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYVMDVWGKTTV 120
Db 83 FRGKTLTVKSSSTAYMQLSLTSEDSAVYFCARSHYIG-----GSYDFDYWGQGTPL 136
QY 121 IVSS 124
Db 137 TVSS 140

RESULT 12
HV11 MOUSE
ID HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Keth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of

antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24:625-637(1981)
-1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00539; AAA38172.1; -.
CC PIR; A02038; G2MS43.
CC HSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS0835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DOMAIN 118 122 D SEGMENT.
CC DOMAIN 123 137 JH2 SEGMENT.
CC DISULFID 41 115 BY SIMILARITY.
CC NON TER 137 137
CC SEQUENCE 137 AA; 15200 MW; ADD5881BP44B8EC9 CRC64;

Query Match 48.3%; Score 325.5; DB 1; Length 137;
Best Local Similarity 49.2%; Pred. No. 3.1e-27;
Matches 61; Conservative 23; Mismatches 31; Indels 9; Gaps 1;

QY 1 LEQSGAEVKPGASVKVSQASGYRFSNFIHVVRQAPGQRFWMGWINPYNKKEPSAK 60
Db 23 LQSGAEIVKPGASVKLSCKASGYTFTSYLHMVWVQPGGLEWIGIPNGYINYNEX 82
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYVMDVWGKTTV 120
Db 83 FRKATLTDKPSSTAYMQLSLTSEDSAVYICARY-----RLGRVFDYWGQGTTL 133
QY 121 IVSS 124
Db 134 TVSS 137

RESULT 13
HV48 MOUSE
ID HV48 MOUSE STANDARD; PRT; 138 AA.
AC P0380;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an Igd-secreting plasmacytoma."
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
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Db 4 LVQSGAEVKKPGSSVKVSKASGCTPERSAIIVWRQAPGGGLEWMMGIVPMFPNNYAK 63
Qy 61 FQDRVTFTADTSANTAYMELRSASDTAVYCYA-RVGPYSWDDSPQDNYMDVWGKGT 119
Db 64 FQGRVTITADESTNTAYMELSSLRSEDTAFYFCAGGYGIY-----SPEEY-----NGGL 112
Qy 120 IVSS 124
Db 113 TVSS 117

RESULT 16
HV1F_HUMAN STANDARD; PRT; 125 AA.
AC P06326;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region Mot.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=86203277; PubMed=3084950;
RX Kojima M., Koide T., Odani S., Ono T.;
RT "Amino acid sequence of the variable region of heavy chain in
RL immunoglobulin (Mot) having unusual papain cleavage sites.";
DR PIR; A02025; HVHUMO.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006985; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT NON_TER 98
FT DOMAIN 99 107 D SEGMENT.
FT NON_TER 107
FT DOMAIN 108 125 J SEGMENT.
FT DISULFID 22 96
FT NON_TER 125 125 BY SIMILARITY.
SQ SEQUENCE 125 AA; 13579 MW; F4C4285D6DF0C8EA CRC64;

Query Match 47.3%; Score 319; DB 1; Length 125;
Best Local Similarity 50.8%; Pred. No. 1.4e-26;
Matches 63; Conservative 19; Mismatches 40; Indels 2; Gaps 1;

Qy 1 LEQSGAEVKKPGASVKYSCKASGYRFSNFIHWVRQAPGQRFEMWGNINPYNGKFSK 60
Db 4 LVQSGAEVKKPGSSARISCKVSGDDFTYDIHWVRQAPGRLWMAVHPSDDRTYGR 63
Qy 61 FQDRVTFTADTSANTAYMELRSASDTAVYCYARVGPYSWDDSPQDNYMDVWGKGT 120
Db 64 SQARFTVTRDSSTTVYMYELTALISADTAIYCYARGAHYS--DTDDSGTSLGPWGQGTLL 121
Qy 121 IVSS 124
Db 122 IVSS 125

RESULT 17
HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MPC 11.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RX Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93708; GVMS11.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 47.2%; Score 318; DB 1; Length 121;
Best Local Similarity 50.0%; Pred. No. 1.7e-26;
Matches 62; Conservative 26; Mismatches 30; Indels 6; Gaps 3;

Qy 1 LEQSGAEVKKPGASVKYSCKASGYRFSNFIHWVRQAPGQRFEMWGNINPYNGKFSK 60
Db 4 LQSGAEVLRPGTSVKISCKAAGTFYNIWGWKRPGLGLEWIGDIPFGGFTINDN 63
Qy 61 FQDRVTFTADTSANTAYMELRSASDTAVYCYARVGPYSWDDSPQDNYMDVWGKGT 120
Db 64 LKGKATLTADTSSTAYIQLSLTSEDSAIYHCAR-GIY-YNSSP----YFDSWGQGTLL 117
Qy 121 IVSS 124
Db 118 TVSS 121

RESULT 18
HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 108A precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RX Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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RESULT 26	
HV10_MOUSE	
ID HV10_MOUSE	STANDARD; PRT; 117 AA.

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AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain V region 145 precursor.
GN IGH-VJ558
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
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CC -----
CC EMBL; J00533; AAA38602.1; -
CC PIR; C90809; HVMS45.
CC HSSP; P01810; 2FBJ.
CC MGD; MGI:96486; Igh-VJ558.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC NON TER 117 117
CC SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;
Query Match 42.6%; Score 287; DB 1; Length 117;
Best Local Similarity 53.7%; Pred. No. 2.9e-23;
Matches 51; Conservative 22; Mismatches 22; Indels 0; Gaps 0;
QY 1 LEOSGAEVKKPCASVKVSCQASGYRFSNFVTHVYRQAPGQRFQFWGWINPYNGKFSK 60
DB 23 LQPGAEVLKPGSVKSSKASGYTFYSYWMWQKRPQGLEWIGNIGIDNSGKTYNEK 82
QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYYCAR 95
DB 83 FKSKATLTVDKPSSTAYMQLSLTSDSAVYYCAR 117
RESULT 27
ID HV05 MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain V region 3 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00536; AAA38605.1; -
CC PIR; A02031; HVMS3.
CC HSSP; P01810; 2FBJ.
CC MGD; MGI:96486; Igh-VJ558.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; IGV.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC NON TER 117 117
CC SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;
Query Match 42.4%; Score 286; DB 1; Length 117;
Best Local Similarity 53.7%; Pred. No. 3.6e-23;
Matches 51; Conservative 21; Mismatches 23; Indels 0; Gaps 0;
QY 1 LEOSGAEVKKPCASVKVSCQASGYRFSNFVTHVYRQAPGQRFQFWGWINPYNGKFSK 60
DB 23 LQPGAEVLKPGSVKSSKASGYTFYSYWMWQKRPQGLEWIGNIGIDNSGKTYNEK 82
QY 61 FQDRVTFADTSANTAYMELSLRSADTAVYYCAR 95
DB 83 FKDKATLTVDKSSSTAYMQLSLTSDSAVYYCAR 117
RESULT 28
ID HV16 MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,

```


Search completed: August 26, 2004, 13:38:01
Job time : 8.34815 secs

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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:32:07 ; Search time 53.5333 Seconds
(without alignments)
770.584 Million cell updates/sec

Title: US-10-016-986-155
Perfect score: 793
Sequence: 1 MWSWVFLPFLSVTTGVHQSQ.....PODNYMDVWGKTTIVSS 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing-first 100 summaries

Database : A Genesep29Jan04:*

- 1: Genesep1980s:*
- 2: Genesep1990s:*
- 3: Genesep2000s:*
- 4: Genesep2001s:*
- 5: Genesep2002s:*
- 6: Genesep2003as:*
- 7: Genesep2003bs:*
- 8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	793	100.0	146	2	AAW01228 VH region
2	793	100.0	146	3	AAAY98285 Modified
3	793	100.0	146	3	AAAY95176 Modified
4	793	100.0	146	7	ADE06734 Human IGG
5	793	100.0	476	7	ABR61564 Human Mab
6	667	84.1	124	2	AAAR54244 Anti-HIV
7	667	84.1	124	2	AAAR75568 VH Fab MT
8	667	84.1	124	2	AAW01227 VH region
9	667	84.1	124	3	AAAY98206 Anti-gp12
10	667	84.1	124	3	AAAY95097 Anti-gp12
11	659	83.1	250	3	AAAY44346 3B3 antiB
12	657	82.8	124	2	AAAR75604 VH Fab H4
13	656	82.7	124	2	AAAR75605 VH Fab H4
14	653	82.3	124	2	AAAR54245 Anti-HIV
15	653	82.3	124	2	AAW01246 VH region
16	653	82.3	124	3	AAAY98207 Anti-gp12
17	653	82.3	124	3	AAAY95098 Anti-gp12
18	650	82.0	124	2	AAAR75607 VH Fab H4
19	650	82.0	124	2	AAAR75608 VH Fab H4
20	649	81.8	124	2	AAAR54246
21	649	81.8	124	2	AAW01247 VH region
22	649	81.8	124	3	AAAY98208 Anti-gp12
23	649	81.8	124	3	AAAY95099 Anti-gp12
24	648	81.7	124	2	AAAR75606 VH Fab H4
25	648	81.7	124	2	AAAR75609 VH Fab H4

26	646	81.5	124	2	AAAR75572	AAar75572	VH Fab 3b
27	645	81.3	124	2	AAAR75570	AAar75570	VH Fab 3b
28	641.5	80.9	124	2	AAAR54335	AAar54335	Anti-HIV
29	641.5	80.9	124	2	AAW01309	AAw01309	VH region
30	641.5	80.9	124	3	AAAY98270	AAy98270	Anti-gp12
31	641.5	80.9	124	3	AAAY95161	AAy95161	Anti-gp12
32	635	80.1	124	2	AAAR75569	AAar75569	VH Fab 3b
33	622.5	78.5	123	2	AAAR75571	AAar75571	VH Fab 3b
34	619	78.1	124	2	AAAR75616	AAar75616	VH Fab M5
35	619	78.1	124	2	AAAR75616	AAar75616	VH Fab M5
36	618	77.9	124	2	AAAR75615	AAar75615	VH Fab M5
37	612	77.2	124	2	AAAR75610	AAar75610	VH Fab M5
38	612	77.2	124	2	AAAR75613	AAar75613	VH Fab M5
39	611	77.0	124	2	AAAR75611	AAar75611	VH Fab M5
40	610	76.9	124	2	AAAR75612	AAar75612	VH Fab M5
41	610	76.9	124	2	AAAR75614	AAar75614	VH Fab M5
42	600	75.7	124	2	AAAR75640	AAar75640	VH Fab H1
43	599	75.5	124	2	AAAR75638	AAar75638	VH Fab H3
44	599	75.5	124	2	AAAR75641	AAar75641	VH Fab H1
45	598	75.4	124	2	AAAR75639	AAar75639	VH Fab H3
46	572.5	72.2	124	2	AAAR54331	AAar54331	Anti-HIV
47	572.5	72.2	124	2	AAW01305	AAw01305	VH region
48	572.5	72.2	124	3	AAAY98266	AAy98266	Anti-gp12
49	572.5	72.2	124	3	AAAY95157	AAy95157	Anti-gp12
50	549.5	69.3	124	2	AAAR54330	AAar54330	Anti-HIV
51	549.5	69.3	124	2	AAAR54336	AAar54336	Anti-HIV
52	549.5	69.3	124	2	AAW01310	AAw01310	VH region
53	549.5	69.3	124	2	AAW01304	AAw01304	VH region
54	549.5	69.3	124	3	AAAY98271	AAy98271	Anti-gp12
55	549.5	69.3	124	3	AAAY98265	AAy98265	Anti-gp12
56	549.5	69.3	124	3	AAAY95156	AAy95156	Anti-gp12
57	549.5	69.3	124	3	AAAY95162	AAy95162	Anti-gp12
58	543.5	68.5	125	2	AAAR54333	AAar54333	Anti-HIV
59	543.5	68.5	125	2	AAAR54268	AAar54268	Anti-HIV
60	543.5	68.5	125	2	AAW01307	AAw01307	VH region
61	543.5	68.5	125	2	AAW01303	AAw01303	VH region
62	543.5	68.5	125	3	AAAY98268	AAy98268	Anti-gp12
63	543.5	68.5	125	3	AAAY98264	AAy98264	Anti-gp12
64	543.5	68.5	125	3	AAAY95159	AAy95159	Anti-gp12
65	543.5	68.5	125	3	AAAY95155	AAy95155	Anti-gp12
66	540.5	68.2	124	2	AAAR54332	AAar54332	Anti-HIV
67	540.5	68.2	124	2	AAW01306	AAw01306	VH region
68	540.5	68.2	124	3	AAAY98267	AAy98267	Anti-gp12
69	540.5	68.2	124	3	AAAY95158	AAy95158	Anti-gp12
70	536.5	67.7	126	2	AAAR54329	AAar54329	Anti-HIV
71	536.5	67.7	126	3	AAAY98263	AAy98263	Anti-gp12
72	536.5	67.7	126	3	AAAY95154	AAy95154	Anti-gp12
73	533.5	67.3	124	2	AAAR54269	AAar54269	Anti-HIV
74	533.5	67.3	124	2	AAW01311	AAw01311	VH region
75	533.5	67.3	124	3	AAAY98272	AAy98272	Anti-gp12
76	533.5	67.3	124	3	AAAY95163	AAy95163	Anti-gp12
77	533.5	67.3	126	2	AAW01302	AAw01302	VH region
78	531.5	67.0	249	2	AAAR77610	AAar77610	Humanised
79	528.5	66.6	139	2	AAAR33953	AAar33953	GH1 varia
80	528.5	66.6	139	2	AAW23753	AAw23753	CDR-graft
81	528.5	66.6	139	3	AAAY56877	AAy56877	GH1 varia
82	522.5	65.9	125	2	AAAR54334	AAar54334	Anti-HIV
83	522.5	65.9	125	2	AAW01308	AAw01308	VH region
84	522.5	65.9	125	3	AAAY98269	AAy98269	Anti-gp12
85	522.5	65.9	125	3	AAAY95160	AAy95160	Anti-gp12
86	522.5	65.9	125	3	AAAR77615	AAar77615	Humanised
87	522	65.8	140	2	AAW21847	AAw21847	Humanised
88	520.5	65.6	249	2	AAAR77611	AAar77611	Humanised
89	510	64.3	140	2	AAW21849	AAw21849	Humanised
90	506	63.8	140	2	AAAR64235	AAar64235	Humanised
91	506	63.8	140	2	AAAR64265	AAar64265	CDR-graft
92	506	63.8	470	5	AAU74296	AAu74296	Anti-huma
93	504	63.6	146	2	AAW22841	AAw22841	Human ant
94	501.5	63.2	137	3	AAAY98847	AAy98847	Humanised
95	500.5	63.1	588	2	AAW71880	AAw71880	Anti-huma
96	500.5	63.1	588	3	AAAB12917	AAb12917	Anti-huma
97	498.5	62.9	135	2	AAAR24107	AAar24107	Humanised
98	498	62.8	140	2	AAW21850	AAw21850	Humanised

CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation
 XX
 XX Sequence 146 AA;

Query Match 100.0%; Score 793; DB 3; Length 146;
 Best Local Similarity 100.0%; Pred. No. 1.4e-68;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWSWVFLFLLSVTTGVHSQVQLVSGAEVKPGASVKSCQASGYRFSNFIHWRQAP 60
 DB 1 MWSWVFLFLLSVTTGVHSQVQLVSGAEVKPGASVKSCQASGYRFSNFIHWRQAP 60

QY 61 GQFEWGWINPYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYCARVGP 120
 DB 61 GQFEWGWINPYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYCARVGP 120

QY 121 YSWDDSPQDNYMDVWGKGTIVSS 146
 DB 121 YSWDDSPQDNYMDVWGKGTIVSS 146

RESULT 3
 AAY95176
 ID AAY95176 standard; protein; 146 AA.
 AC AAY95176;
 XX
 XX 30-JUN-2000 (first entry)
 DE Modified heavy chain variable region amino acid sequence.

XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 XX Synthetic.
 XX AU948756-A.
 PN 17-FEB-2000.

XX 16-SEP-1999; 99AU-00048756.
 XX 16-SEP-1999; 99AU-00048756.
 XX (SCRI) SCRIPPS RES INST.
 XX Burton DR, Barbas CF, Lerner RA;
 XX WPI; 2000-293393/26.

XX Novel human monoclonal antibodies which immunoreact with and neutralize
 PT human immunodeficiency virus useful for treating HIV infections.

XX Example 4; Page 111; 366pp; English.

XX The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and

CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV
 XX
 XX Sequence 146 AA;

Query Match 100.0%; Score 793; DB 3; Length 146;
 Best Local Similarity 100.0%; Pred. No. 1.4e-68;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWSWVFLFLLSVTTGVHSQVQLVSGAEVKPGASVKSCQASGYRFSNFIHWRQAP 60
 DB 1 MWSWVFLFLLSVTTGVHSQVQLVSGAEVKPGASVKSCQASGYRFSNFIHWRQAP 60

QY 61 GQFEWGWINPYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYCARVGP 120
 DB 61 GQFEWGWINPYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYCARVGP 120

QY 121 YSWDDSPQDNYMDVWGKGTIVSS 146
 DB 121 YSWDDSPQDNYMDVWGKGTIVSS 146

RESULT 4
 ADE06734
 ID ADE06734 standard; protein; 146 AA.
 XX
 AC ADE06734;
 XX
 XX 29-JAN-2004 (first entry)
 DE Human IGG Fab b12 heavy chain protein SEQ ID NO:4.

XX hybrid polypeptide; protein aggregation; prion polypeptide;
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant;
 KW cerebroprotective; antiparkinsonian; cyostatic; nephrotropic; cardiant;
 KW antiinflammatory; antiarteriosclerotic; gene therapy;
 KW Creutzfeldt-Jakob disease; scrapie and bovine spongiform encephalopathy;
 KW Alzheimer's disease; Type II diabetes; Huntington's disease;
 KW immunoglobulin amyloidosis; amyloidosis; chronic inflammatory disease;
 KW amyotrophic lateral sclerosis; Pick's disease; Parkinson's disease;
 KW Frontotemporal dementia; multiple myeloma; plasma cell dyscrasia;
 KW familial amyloidotic polyneuropathy; medullary carcinoma;
 KW chronic renal failure; congestive heart failure; chronic inflammation;
 KW atherosclerosis; human.

XX Homo sapiens.

XX WO2003085086-A2.

XX 16-OCT-2003.

XX 08-APR-2003; 2003WO-US010856.

XX 09-APR-2002; 2002US-0371610P.

XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Williamson RA, Moroncini G;
 XX WPI: 2003-877028/81.
 XX N-PSDB; ADE06733.
 XX
 XX New motif-grafted hybrid polypeptides binding to the infectious form of a
 XX prion, useful for diagnosing or treating diseases of protein aggregation
 XX or conformation, e.g. amyloidosis, Alzheimer's disease, renal failure or
 XX diabetes.
 XX
 XX Claim 37; SEQ ID NO 4; 115pp; English.
 XX
 XX The present invention describes a hybrid polypeptide (I) comprising: (a)
 XX a polypeptide motif containing a sufficient number of contiguous amino
 XX acid residues from a polypeptide associated with a disease of protein
 XX aggregation or conformation to bind an aggregating form of the
 XX polypeptide or to a disease-associate conformer of the polypeptide; and
 XX (b) an additional amino acids from a polypeptide other than the
 XX polypeptide from which the motif is derived, where the resulting hybrid
 XX polypeptide binds with greater affinity to a disease causing or
 XX infectious conformer of the polypeptide than is the source of the
 XX polypeptide motif compared to a benign form of the polypeptide. Also
 XX described: (1) a nucleic acid molecule encoding (I); (2) a vector
 XX comprising the nucleic acid molecule; (3) a cell comprising the vector;
 XX (4) detecting an isoform or a PfSC form of a prion polypeptide or a
 XX polypeptide associated with a disease of protein aggregation, in a sample
 XX ; (5) a solid support comprising a plurality of polypeptides described
 XX above; (6) detecting cells that contain a protein conformer associated
 XX with a disease of protein aggregation; (7) preparing a hybrid molecule
 XX that specifically interacts with one conformer of a protein involved in
 XX the disease mentioned above; and (8) an anti-idiotypic antibody that
 XX specifically binds to an infectious form of a prion protein. (I) has
 XX neuroprotective, neurotropic, antidiabetic, anticonvulsant,
 XX cerebroprotective, antiparkinsonian, cytoskeletal, neurotropic, cardiant,
 XX antiinflammatory and antiarteriosclerotic activities, and can be used in
 XX gene therapy. The composition and methods of the present invention can be
 XX used in diagnosing or treating diseases of protein aggregation or
 XX conformation, such as Creutzfeldt-Jakob disease, scrapie and bovine
 XX spongiform encephalopathy, Alzheimer's disease, Type II diabetes,
 XX Huntington's disease, immunoglobulin amyloidosis, reactive amyloidosis
 XX associated with chronic inflammatory disease, hereditary systemic
 XX amyloidosis associated with autosomal dominant inheritance of variant
 XX transthyretin gene, amyotrophic lateral sclerosis, Pick's disease,
 XX Parkinson's disease, frontotemporal dementia, multiple myeloma, plasma
 XX cell dyscrasias, familial amyloidotic polyneuropathy, medullary carcinoma
 XX of thyroid, chronic renal failure, congestive heart failure, senile
 XX cardiac and systemic amyloidosis, chronic inflammation, atherosclerosis
 XX or familial amyloidosis. The present sequence is used in the
 XX exemplification of the present invention.
 XX
 XX Sequence 146 AA;
 XX
 XX Query Match 100.0%; Score 793; DB 7; Length 146;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-68;
 XX Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 M E W S W F L F L S V T T G V H S Q V L V Q S G A E V K P G A S V K V S C Q A S G Y R F S N F V I H W R Q A P 60
 XX Db 1 M E W S W F L F L S V T T G V H S Q V L V Q S G A E V K P G A S V K V S C Q A S G Y R F S N F V I H W R Q A P 60
 XX
 XX QY 61 G Q R F E W G W I N P Y N G N K E F S A K F Q D R V T F T A D T S A N T A Y M E L S R S A D T A V Y Y C A R V G P 120
 XX Db 61 G Q R F E W G W I N P Y N G N K E F S A K F Q D R V T F T A D T S A N T A Y M E L S R S A D T A V Y Y C A R V G P 120
 XX
 XX QY 121 Y S W D D S P Q D N Y M D V N G K G T T V I V S S 146
 XX Db 121 Y S W D D S P Q D N Y M D V N G K G T T V I V S S 146
 XX
 XX RESULT 5
 XX ABR61564
 XX ID ABR61564 standard; protein; 476 AA.

XX ABR61564;
 XX AC 15-JAN-2004 (first entry)
 XX DT Human MAb IgG1b12 heavy chain.
 XX DE Adeno-associated virus; rAAV; IgG1b12; ScFvX5; anti-HIV; antibacterial;
 XX KW antirheumatic; antiarthritic; cytostatic; sedative; antiinflammatory;
 XX KM neuroprotective; gene therapy; vaccine; antibody; Mab.
 XX XX
 XX OS Homo sapiens.
 XX XX
 XX PN WC2003087324-A2.
 XX XX
 XX PD 23-OCT-2003.
 XX XX
 XX PF 09-APR-2003; 2003WO-US010865.
 XX XX
 XX PR 09-APR-2002; 2002US-0371501P.
 XX XX
 XX PA (CHIL-) CHILDRENS HOSPITAL INC.
 XX XX
 XX PI Clark KB; Johnson PR;
 XX XX
 XX WPI: 2003-833721/77.
 XX DR N-PSDB; ACF58045.
 XX XX
 XX PT New recombinant adeno-associated virus (rAAV)/IgG1b12 or rAAV/ScFvX5
 XX genome, useful for preventing or treating viral infections (e.g. HIV),
 XX bacterial infections or other chronic disease states (e.g. cancer,
 XX inflammation or kuru).
 XX XX
 XX Example 1; Page 35-37; Opp; English.
 XX
 XX The invention relates to a recombinant adeno-associated virus (rAAV)/
 XX IgG1b12 or rAAV/ScFvX5 genome. The rAAV is useful for gene delivery,
 XX particularly in delivering antibody genes to target cells in mammals. The
 XX antibodies may be used to prevent and/or treat viral infections
 XX (particularly HIV), bacterial infections and other chronic disease states
 XX (e.g. cancer, rheumatoid arthritis, inflammation, fatal familial
 XX insomia, kuru, Mad Cow Disease or Alpers syndrome). The present sequence
 XX represents the human monoclonal antibody (Mab) IgG1b12 heavy chain
 XX
 XX Sequence 476 AA;
 XX
 XX Query Match 100.0%; Score 793; DB 7; Length 476;
 XX Best Local Similarity 100.0%; Pred. No. 5.4e-68;
 XX Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 M E W S W F L F L S V T T G V H S Q V L V Q S G A E V K P G A S V K V S C Q A S G Y R F S N F V I H W R Q A P 60
 XX Db 1 M E W S W F L F L S V T T G V H S Q V L V Q S G A E V K P G A S V K V S C Q A S G Y R F S N F V I H W R Q A P 60
 XX
 XX QY 61 G Q R F E W G W I N P Y N G N K E F S A K F Q D R V T F T A D T S A N T A Y M E L S R S A D T A V Y Y C A R V G P 120
 XX Db 61 G Q R F E W G W I N P Y N G N K E F S A K F Q D R V T F T A D T S A N T A Y M E L S R S A D T A V Y Y C A R V G P 120
 XX
 XX QY 121 Y S W D D S P Q D N Y M D V N G K G T T V I V S S 146
 XX Db 121 Y S W D D S P Q D N Y M D V N G K G T T V I V S S 146
 XX
 XX RESULT 6
 XX AAR54244
 XX ID AAR54244 standard; protein; 124 AA.
 XX XX
 XX AC AAR54244;
 XX XX
 XX DT 25-MAR-2003 (revised)
 XX DT 10-NOV-1994 (first entry)
 XX XX
 XX DE Anti-HIV gp120 immunoglobulin heavy chain variable region b4.

Db 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKSFSAK 60
 QY 83 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
 Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
 QY 143 IVSS 146
 Db 121 IVSS 124
 RESULT 8
 ID AAW01227
 XX AAW01227 standard; protein, 124 AA.
 AC AAW01227;
 XX 27-JAN-1997 (first entry)
 XX VH region of HIV neutralising MAb, clones b4 and b12.
 XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
 KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 XX Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..27
 FT /label= FR1
 FT Region 28..32
 FT /label= CDR1
 FT Region 33..46
 FT /label= FR2
 FT Region 47..63
 FT /label= CDR2
 FT Region 64..95
 FT /label= FR3
 FT Region 96..113
 FT /label= CDR3
 FT Region 114..124
 FT /label= FR4
 XX WO9602273-A1.
 XX 01-FEB-1996.
 XX 11-JUL-1995; 95WO-US008743.
 XX 18-JUL-1994; 94US-00276852.
 XX (SCRI) SCRIPPS RES INST.
 XX Burton DR, Barbas CF, Lerner RA;
 XX WPI; 1996-179601/18.
 XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
 XX immunotherapy and detection of HIV infection.
 XX Claim 9; Fig 10; 366pp; English.
 CC This sequence represents the heavy chain variable region (VH) of a
 CC monoclonal antibody (MAb) which is immunoreactive with HIV glycoprotein
 CC gp120 and is capable of neutralising HIV. This sequence represents the
 CC sequence of clones b4 and b12. The MAb has the capacity to reduce HIV
 CC infectivity titre in an in vivo virus infectivity assay by 50 % at a
 CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
 CC preferentially over the precursor gp160. This sequence forms the heavy
 CC chain component of MAb's with the light chain sequences given in
 CC AAW01273, AAW01275-76, AAW01293, and AAW01299-300. The MAb may
 CC be used for determining immunocompetence of a human anti-HIV antibody and

CC in the detection of HIV infection
 XX Sequence 124 AA;
 SQ Query Match 84.1%; Score 667; DB 2; Length 124;
 Best Local Similarity 99.2%; Pred. No. 1.6e-56;
 Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 23 LVQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKSFSAK 82
 Db 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKSFSAK 60
 QY 83 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
 Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
 QY 143 IVSS 146
 Db 121 IVSS 124
 RESULT 9
 ID AAY98206
 XX AAY98206 standard; protein, 124 AA.
 AC AAY98206;
 XX 04-JUL-2000 (first entry)
 XX Anti-gp120 antibody heavy chain variable region from clone b4.
 XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX Homo sapiens.
 XX AU9948754-A.
 XX 17-FEB-2000.
 XX 16-SEP-1999; 99AU-00048754.
 XX 16-SEP-1999; 99AU-00048754.
 XX (SCRI) SCRIPPS RES INST.
 XX Burton DR, Barbas CF, Lerner RA;
 XX WPI; 2000-246867/22.
 XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
 XX (HIV) used for providing passive immunotherapy to HIV are specific for
 XX glycoprotein-120.
 XX Claim 1; Fig 10; 374pp; English.
 CC This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity
 CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
 CC production of the antibody comprises: (a) providing a first
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 CC (which does not comprise the sequence represented by AAY98206) and a
 CC second polynucleotide encoding a light chain immunoglobulin amino acid
 CC sequence; (b) inserting the first and second polynucleotide sequences
 CC into a host cell; (c) maintaining the host cell in conditions which allow
 CC the amino acid sequences encoded by the polynucleotides to be expressed
 CC in the host cell; and (d) isolating the antibody comprising the heavy and
 CC light chain immunoglobulin amino acid sequences from the host cell. The
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive

CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used for
 CC neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting HIV
 CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation. Note: The present sequence is specifically not claimed
 XX
 SQ Sequence 124 AA;

Query Match 84.1%; Score 667; DB 3; Length 124;
 Best Local Similarity 99.2%; Pred. No. 1.6e-56;
 Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 LVOSGAEVKPGASVKVSCQASGYRFSNFIHWRQAPGQRFENWGMINPYNKKEFSAX 82
 DB 1 LEOSGAEVKPGASVKVSCQASGYRFSNFIHWRQAPGQRFENWGMINPYNKKEFSAX 60

QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
 DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
 DB 121 IVSS 124

RESULT 11
 AAY95097
 ID AAY95097 standard; protein; 124 AA.
 AC AAY95097;
 XX 30-JUN-2000 (first entry)
 DT Anti-gp120 antibody heavy chain variable region from clone b4.
 DE
 XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 XX
 OS Homo sapiens.
 XX AU948756-A.
 XX 17-FEB-2000.
 XX 16-SEP-1999; 99AU-00048756.
 XX 16-SEP-1999; 99AU-00048756.
 XX (SCRI) SCRIPPS RES INST.
 XX Burton DR, Barbas CF, Lerner RA;
 XX WPI; 2000-293393/26.
 XX Novel human monoclonal antibodies which immunoreact with and neutralize
 XX human immunodeficiency virus useful for treating HIV infections.
 XX Example 9; Fig 10; 366pp; English.
 XX The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to

CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50% at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of the
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV
 XX
 SQ Sequence 124 AA;

Query Match 84.1%; Score 667; DB 3; Length 124;
 Best Local Similarity 99.2%; Pred. No. 1.6e-56;
 Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 LVOSGAEVKPGASVKVSCQASGYRFSNFIHWRQAPGQRFENWGMINPYNKKEFSAX 82
 DB 1 LEOSGAEVKPGASVKVSCQASGYRFSNFIHWRQAPGQRFENWGMINPYNKKEFSAX 60

QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
 DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
 DB 121 IVSS 124

RESULT 11
 AAY44346
 ID AAY44346 standard; protein; 250 AA.
 AC AAY44346;
 XX 14-MAR-2000 (first entry)
 DT 3B3 antibody.
 DE
 XX 3B3 antibody; immunotoxin; variable fragment; Fv; gp120 coat protein;
 KW exotoxin; PE38; Human immunodeficiency virus type 1; HIV-1; specificity;
 KW combinatorial phage display library; bone marrow RNA; connector peptide;
 KW cytotoxic moiety; transformed cell line; transplant; quantify.
 XX
 OS Homo sapiens.
 XX Key
 XX Key
 XX Peptide
 XX 129..143
 XX /label= Linker peptide
 XX /note= "Links VH and VL regions of 3B3 antibody"
 XX WO9964073-A2.
 XX 16-DEC-1999.
 XX 08-JUN-1999; 99WO-US012909.
 XX 11-JUN-1998; 98US-0088860P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PA Pastan IH, Bera TK, Kennedy PE, Berger EA, Barbas CF;
 XX PI WPI; 2000-105833/09.
 XX DR N-PSDB; AAZ29448.
 XX DR Novel recombinant immunotoxin directed against the HIV- 1 gp120 coat
 FT protein useful for treating HIV-1 infections.
 FT PS Claim 17; Page 47; 50pp; English.
 XX CC The present amino acid sequence is the variable fragment (Fv) of 3B3
 CC antibody, isolated from a combinatorial phage display library constructed
 CC from bone marrow RNA of an infected individual. It is used in a novel
 CC chimeric immunotoxin, that comprises an anti-gp120 antibody, having
 CC binding specificity to 3B3(Fv) antibody, that is attached by a connector
 CC peptide to a cytotoxic moiety, PE38 derived from P.aeruginosa. The
 CC chimeric immunotoxin is used in the treatment of HIV-1 infections. It is
 CC capable of specifically targeting and killing cells displaying HIV-1
 CC gp120 coat protein. They can be used ex vivo to reduce and/or eliminate
 CC the HIV viral load in the infected cells. It can also be used in
 CC establishing transformed cell lines derived from HIV-infected sources.
 CC The immunotoxins can also be used for detecting the presence or absence
 CC and for quantifying the infected cells
 XX SQ Sequence 250 AA;

Query Match 83.1%; Score 659; DB 3; Length 250;
 Best Local Similarity 95.3%; Pred. No. 2.2e-55;
 Matches 121; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 20 QVQLVQSGAEVKPKGASVKVSCQASGYRFSNFTVHWVROAPGQRFPEWMGWINPYNGKKEF 79
 DB 2 QVLEQSGAEVKPKGASVKVSCQASGYRFSNFTVHWVROAPGQRFPEWMGWINPYNGKKEF 61

QY 80 SAKFQDRVTTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKG 139
 DB 62 SAKFQDRVTTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKG 121

QY 140 TTVIVSS 146
 DB 122 TTVIVSS 128

RESULT 12
 AAR75604
 ID AAR75604 standard; protein; 124 AA.
 XX AC AAR75604;
 XX DT 11-MAR-1996 (first entry)
 XX DE VH Fab H4H1-1 binds to gp120.
 XX KW Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab;
 KW immunoreaction; neutralisation; passive immunotherapy.
 XX OS Synthetic.

Key Location/Qualifiers
 FT Region 1..27
 FT /label= FR1
 FT Region 28..32
 FT /label= CDR1
 FT Region 33..46
 FT /label= FR2
 FT Region 47..63
 FT /label= CDR2
 FT Region 64..95
 FT /label= FR3

FT Region 96..113
 FT /label= CDR3
 FT Region 114..124
 FT /label= FR4
 XX WO9511317-A1.
 XX 27-APR-1995.
 XX 19-OCT-1994; 94WO-US011907.
 XX 19-OCT-1993; 93US-00139409.
 XX 26-APR-1994; 94US-00233619.
 XX 19-SEP-1994; 94US-00308841.
 XX (SCRI) SCRIPPS RES INST.
 XX Barbas CF, Burton DR, Lerner RA;
 WPI; 1995-170235/22.
 XX Synthetic human neutralising monoclonal antibodies to human
 FT immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
 FT induced disease.
 XX Example 4B1; Fig 7; 249pp; English.
 XX The sequences given in AAR75604-09 represent human Fab's comprising
 CC variable chain heavy regions (VH), which bind to HIV gp120. The six amino
 CC acids which comprise CDR1 have been randomised with 3 of the six CDR1
 CC sequences containing the preferred His residue as the first residue of
 CC CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
 CC used in the production of a human monoclonal antibody (Mab) which is
 CC capable of immunoreacting with, and neutralising HIV. The Mab's are
 CC capable of reducing HIV infectivity titre in an in vitro virus
 CC infectivity assay by 5% at a concentration of <100 ng of antibody per
 CC ml. They can be used to provide passive immunotherapy to HIV in a human.
 CC They neutralise HIV more effectively than antibodies selected from non-
 CC randomised combinatorial libraries
 XX SQ Sequence 124 AA;

Query Match 82.8%; Score 657; DB 2; Length 124;
 Best Local Similarity 96.8%; Pred. No. 1.5e-55;
 Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 23 LVQSGAEVKPKGASVKVSCQASGYRFSNFTVHWVROAPGQRFPEWMGWINPYNGKKEFSK 82
 DB 1 LEQSGAEVKPKGASVKVSCQASGYRFSNFTVHWVROAPGQRFPEWMGWINPYNGKKEFSK 60

QY 83 FQDRVTTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 142
 DB 61 FQDRVTTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 143 IVSS 146
 DB 121 IVSS 124

RESULT 13
 AAR75605
 ID AAR75605 standard; protein; 124 AA.
 XX AC AAR75605;
 XX DT 11-MAR-1996 (first entry)
 XX DE VH Fab H4H1-3 binds to gp120.
 XX KW Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab;
 KW immunoreaction; neutralisation; passive immunotherapy.
 XX OS Synthetic.

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OS Synthetic.
XX Key Location/Qualifiers
XX FT Region 1. .27
XX FT Region /label= FR1
XX FT Region 28. .32
XX FT Region /label= CDR1
XX FT Region 33. .46
XX FT Region /label= FR2
XX FT Region 47. .63
XX FT Region /label= CDR2
XX FT Region 64. .95
XX FT Region /label= FR3
XX FT Region 96. .113
XX FT Region /label= CDR3
XX FT Region 114. .124
XX FT Region /label= FR4
XX PN WO9511317-A1.
XX DD 27-APR-1995.
XX PF 19-OCT-1994; 94WO-US011907.
XX PR 19-OCT-1993; 93US-00139409.
XX PR 26-APR-1994; 94US-00233619.
XX PR 19-SEP-1994; 94US-00308841.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Burton DR, Lerner RA;
XX PI WPI; 1995-170235/22.
XX DR Synthetic human neutralising monoclonal antibodies to human
XX FT immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
XX FT induced disease.
XX PS Example 4B1; Fig 7; 249pp; English.
XX CC The sequences given in AAR75604-09 represent human Fab's comprising
XX CC variable chain heavy regions (VH), which bind to HIV gp120. The six amino
XX CC acids which comprise CDR1 have been randomised with 3 of the six CDR1
XX CC sequences containing the preferred His residue as the first residue of
XX CC CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
XX CC used in the production of a human monoclonal antibody (WAB) which is
XX CC capable of immunoreacting with, and neutralising HIV. The Mab's are
XX CC capable of reducing HIV infectivity titre in an in vitro virus
XX CC infectivity assay by 50% at a concentration of <100 ng of antibody per
XX CC ml. They can be used to provide passive immunotherapy to HIV in a human.
XX CC They neutralise HIV more effectively than antibodies selected from non-
XX CC randomised combinatorial libraries
XX SX Sequence 124 AA;
XX Query Match 82.7%; Score 656; DB 2; Length 124;
XX Best Local Similarity 96.8%; Pred. No. 1.9e-55;
XX Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRAQPGQRFEMWGWINPYNGNKEFSAK 82
XX DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRAQPGQRFEMWGWINPYNGNKEFSAK 60
XX QY 83 FQDRVTFADTSAANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
XX DB 61 FQDRVTFADTSAANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
XX QY 143 IVSS 146
XX DB 121 IVSS 124
XX RESULT 14

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AAR54245
ID AAR54245 standard; protein; 124 AA.
XX AC AAR54245;
XX DT 25-MAR-2003 (revised)
XX DT 10-NOV-1994 (first entry)
XX DE Anti-HIV gp120 immunoglobulin heavy chain variable region b7.
XX KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
XX KW neutralisation; monoclonal antibody; heavy chain; variable region;
XX KW framework region; complementarity determining region.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Region 1. .27
XX FT Region /label= FR1
XX FT Region 28. .32
XX FT Region /label= CDR1
XX FT Region 33. .46
XX FT Region /label= FR2
XX FT Region 47. .63
XX FT Region /label= CDR2
XX FT Region 64. .95
XX FT Region /label= FR3
XX FT Region 96. .113
XX FT Region /label= CDR3
XX FT Region 114. .124
XX FT Region /label= FR4
XX PN WO9407922-A1.
XX DD 14-APR-1994.
XX PF 30-SEP-1993; 93WO-US009328.
XX PR 30-SEP-1992; 92US-00954148.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Burton DR, Barbas CF, Lerner RA;
XX DR WPI; 1994-135516/16.
XX PT New human monoclonal antibodies neutralising HIV - react with gp120 or
XX PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
XX PT diagnosis and for passive immuno-therapy.
XX PS Claim 1; Page 164; 248pp; English.
XX CC Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
XX CC using primers specific for heavy and light chain variable regions. The
XX CC amplification products were inserted into a dicistronic vector to produce
XX CC a library of fragments. E.coli XLI Blue cells were transformed with the
XX CC library. Filamentous phage were produced which expressed the Mab regions
XX CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
XX CC immunoreactive clones. The heavy chain VH region sequence AAR54245
XX CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)
XX SX Sequence 124 AA;
XX Query Match 82.3%; Score 653; DB 2; Length 124;
XX Best Local Similarity 96.0%; Pred. No. 3.7e-55;
XX Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRAQPGQRFEMWGWINPYNGNKEFSAK 82
XX DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRAQPGQRFEMWGWINPYNGNKEFSAK 60
XX QY 83 FQDRVTFADTSAANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 142

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Db 61 FQDRVTFADTADTANTAYMELSLRSADTAIYCARVGPTWDDSPQDNYMDVMGKTKV 120
 QY 143 IVSS 146
 ||||
 Db 121 IVSS 124

RESULT 15
 AAW01246
 ID AAW01246 standard; protein; 124 AA.
 XX
 AC AAW01246;
 XX
 DT 28-JAN-1997 (first entry)
 XX
 DE VH region of HIV neutralising MAb, IgG1 b7.
 XX
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
 KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..27
 FT /label= FR1
 FT Region 28..32
 FT /label= CDR1
 FT Region 33..46
 FT /label= FR2
 FT Region 47..63
 FT /label= CDR2
 FT Region 64..95
 FT /label= FR3
 FT Region 96..113
 FT /label= CDR3
 FT Region 114..124
 FT /label= FR4
 XX
 FN WO9602273-A1.
 XX
 PD 01-FEB-1996.
 XX
 PF 11-JUL-1995; 95WO-US008743.
 XX
 PR 18-JUL-1994; 94US-00276852.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 XX
 PS WPI; 1996-179601/18.
 XX
 DR Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
 PT immuno:therapy and detection of HIV infection.
 XX
 PS Example; Fig 10; 366pp; English.
 XX
 CC The sequences given in AAW01233-60 represent the heavy chain variable
 CC regions (VH) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JH6 gene
 CC clone, b7. A MAB containing this VH sequence has the capacity to reduce
 CC HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a
 CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
 CC preferentially over the precursor gp160. The MAB may be used for
 CC determining immunocompetence of a human anti-HIV antibody and in the
 CC detection of HIV infection
 XX
 SQ Sequence 124 AA;
 Query Match 82.3%; Score 653; DB 2; Length 124;

Best Local Similarity 96.0%; Pred. No. 3.7e-55;
 Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFVIHWVRQAPGQRFEMWGINPYNNGKFSAK 82
 ||||
 Db 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVIHWVRQAPGQRFEMWGINPYNNGKFSAK 60
 ||||

QY 83 FQDRVTFADTADTANTAYMELSLRSADTAIYCARVGPTWDDSPQDNYMDVMGKTKV 142
 ||||
 Db 61 FQDRVTFADTADTANTAYMELSLRSADTAIYCARVGPTWDDSPQDNYMDVMGKTKV 120
 ||||

QY 143 IVSS 146
 ||||
 Db 121 IVSS 124

RESULT 16
 AAY98207
 ID AAY98207 standard; protein; 124 AA.
 XX
 AC AAY98207;
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Anti-gp120 antibody heavy chain variable region from clone b7.
 XX
 KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX
 OS Homo sapiens.
 XX
 PN AU9948754-A.
 XX
 PD 17-FEB-2000.
 XX
 PF 16-SEP-1999; 99AU-00048754.
 XX
 PR 16-SEP-1999; 99AU-00048754.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 XX
 PS WPI; 2000-246867/22.
 XX
 DR Human neutralizing monoclonal antibodies to human immunodeficiency virus
 PT (HIV) used for providing passive immunotherapy to HIV are specific for
 PT glycoprotein-120.
 XX
 PS Example 9; Fig 10; 374pp; English.
 XX
 CC This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity
 CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
 CC production of the antibody comprises: (a) providing a first
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 CC (which does not comprise the sequence represented by AAY98206) and a
 CC second polynucleotide encoding a light chain immunoglobulin amino acid
 CC sequence; (b) inserting the first and second polynucleotide sequences
 CC into a host cell; (c) maintaining the host cell in conditions which allow
 CC the amino acid sequences encoded by the polynucleotides to be expressed
 CC in the host cell; and (d) isolating the antibody comprising the heavy and
 CC light chain immunoglobulin amino acid sequences from the host cell. The
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used for
 CC neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting HIV

CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation
 CC
 SQ Sequence 124 AA;

Query Match 82.3%; Score 653; DB 3; Length 124;
 Best Local Similarity 96.0%; Pred. No. 3.7e-55;
 Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEPSAK 82
 DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEPSAK 60

QY 83 FQDRVTFDTADTSANTAYMELRSLSADTAIYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
 DB 61 FQDRVTFDTADTSANTAYMELRSLSADTAIYCARVGPYTWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
 DB 121 IVSS 124

RESULT 18
 AAY95098
 ID AAY95098 standard; protein; 124 AA.
 XX AC AAY95098;
 XX DT 30-JUN-2000 (first entry)
 XX DE Anti-gp120 antibody heavy chain variable region from clone b7.
 XX KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 XX KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 XX KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 XX OS Homo sapiens.
 XX PN AU9948756-A.
 XX PD 17-FEB-2000.
 XX PF 16-SEP-1999; 99AU-00048756.
 XX PR 16-SEP-1999; 99AU-00048756.
 XX PA (SCRI) SCRIPPS RES INST.
 XX PI Burton DR, Barbas CF, Lerner RA;
 XX DR WPI; 2000-293393/26.
 XX PT Novel human monoclonal antibodies which immunoreact with and neutralize
 XX PT human immunodeficiency virus useful for treating HIV infections.
 XX PS Example 9; Fig 10; 366pp; English.
 XX CC The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and

CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp1 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV
 CC
 SQ Sequence 124 AA;

Query Match 82.3%; Score 653; DB 3; Length 124;
 Best Local Similarity 96.0%; Pred. No. 3.7e-55;
 Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEPSAK 82
 DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEPSAK 60

QY 83 FQDRVTFDTADTSANTAYMELRSLSADTAIYCARVGPYSWDDSPQDNYMDVWGKGTIV 142
 DB 61 FQDRVTFDTADTSANTAYMELRSLSADTAIYCARVGPYTWDDSPQDNYMDVWGKGTIV 120

QY 143 IVSS 146
 DB 121 IVSS 124

RESULT 18
 AAR75607
 ID AAR75607 standard; protein; 124 AA.
 XX AC AAR75607;
 XX DT 11-MAR-1996 (first entry)
 XX DE VH Fab H4H1-6 binds to gp120.
 XX KW Human; Fab; variable chain; heavy; light; region; VH; HIV; gp120;
 XX KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; MAB;
 XX KW immunoreaction; neutralisation; passive immunotherapy.
 XX OS Synthetic.
 XX PH Key
 XX FT Region Location/Qualifiers
 XX FT 1..27 /label= FR1
 XX FT 28..32 /label= CDR1
 XX FT 33..46 /label= FR2
 XX FT 47..63 /label= CDR2
 XX FT 64..95 /label= FR3
 XX FT 96..113 /label= CDR3
 XX FT 114..124 /label= FR4
 XX WO9511317-A1.
 XX PN

XX Anti-HIV gp120 immunoglobulin heavy chain variable region b21.
 DE Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 XX neutralisation; monoclonal antibody; heavy chain; variable region;
 KW framework region; complementarity determining region.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..27
 FT /label= FR1
 FT Region 28..32
 FT /label= CDR1
 FT Region 33..46
 FT /label= FR2
 FT Region 47..63
 FT /label= CDR2
 FT Region 64..95
 FT /label= FR3
 FT Region 96..113
 FT /label= CDR3
 FT Region 114..124
 FT /label= FR4

XX WO9407922-A1.

XX 14-APR-1994.

XX 30-SEP-1993; 93WO-US009328.

XX 30-SEP-1992; 92US-00954148.

XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;

XX WPI; 1994-135516/16.

XX New human monoclonal antibodies neutralising HIV - react with gp120 or
 PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
 PT diagnosis and for passive immuno-therapy.

XX Claim 1; Page 165; 248pp; English.

XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
 CC using primers specific for heavy and light chain variable regions. The
 CC amplification products were inserted into a dicistronic vector to produce
 CC a library of fragments. E.coli Xli Blue cells were transformed with the
 CC library. Filamentous phage were produced which expressed the MAb regions
 CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
 CC immunoreactive clones. The heavy chain VH region sequence AAR54246
 CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 124 AA;

Query Match 81.8%; Score 649; DB 2; Length 124;
 Best Local Similarity 95.2%; Pred. No. 8.9e-55;
 Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFVHWRQAPGQRFEMWGINPYNKKEFSK 82
 DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHWRQAPGQRFEMWGINPYNKKEFSK 60

QY 83 FQDVTETADTSANTAYWEILRSADTAYVCARYGPISWDDSPQDNYMDVWGKTTV 142
 DB 61 FQDVTETADTSANTAYWEILRSADTAYVCARYGPISWDDSPQDNYMDVWGKTKV 120

QY 143 IVSS 146

DB 121 IVSS 124

RESULT 21
 AAW01247
 ID AAW01247 standard; protein; 124 AA.

XX AAW01247;

XX 28-JAN-1997 (first entry)

XX VH region of HIV neutralising MAb, IgG1 b21.

XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
 KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 XX anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..27
 FT /label= FR1
 FT Region 28..32
 FT /label= CDR1
 FT Region 33..46
 FT /label= FR2
 FT Region 47..63
 FT /label= CDR2
 FT Region 64..95
 FT /label= FR3
 FT Region 96..113
 FT /label= CDR3
 FT Region 114..124
 FT /label= FR4

XX WO9602273-A1.

XX 01-FEB-1996.

XX 11-JUL-1995; 95WO-US008743.

XX 18-JUL-1994; 94US-00276852.

XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;

XX WPI; 1996-179601/18.

XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
 PT immuno:therapy and detection of HIV infection.

XX Example; Fig 10; 368pp; English.

XX The sequences given in AAW01233-60 represent the heavy chain variable
 CC regions (VH) of a series of monoclonal antibodies (MAb's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JH6 gene
 CC clone, b21. A MAb containing this VH sequence has the capacity to reduce
 CC HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a
 CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
 CC preferentially over the precursor gp160. The MAb may be used for
 CC determining immunocompetence of a human anti-HIV antibody and in the
 CC detection of HIV infection

XX Sequence 124 AA;

Query Match 81.8%; Score 649; DB 2; Length 124;
 Best Local Similarity 95.2%; Pred. No. 8.9e-55;
 Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFVHWRQAPGQRFEMWGINPYNKKEFSK 82
 DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFVHWRQAPGQRFEMWGINPYNKKEFSK 60

QY 83 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142
 Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYTWDDSPQDNYMDVWGKTKV 120
 QY 143 IVSS 146
 Db 121 IVSS 124

RESULT 22
 AAY98208
 ID AAY98208 standard; protein; 124 AA.
 XX AC AAY98208;
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Anti-gp120 antibody heavy chain variable region from clone b21.
 XX
 KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX
 OS Homo sapiens.
 CS
 FN AU9948754-A.
 XX
 PD 17-FEB-2000.
 XX
 PF 16-SEP-1999; 99AU-00048754.
 XX
 PR 16-SEP-1999; 99AU-00048754.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 XX
 DR WPI; 2000-246867/22.
 XX
 PT Human neutralizing monoclonal antibodies to human immunodeficiency virus
 PT (HIV) used for providing passive immunotherapy to HIV are specific for
 PT glycoprotein-120.
 XX
 PS Example 9; Fig 10; 374pp; English.
 XX

This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity
 CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
 CC production of the antibody comprises: (a) providing a first
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 CC (which does not comprise the sequence represented by AAY98206) and a
 CC second polynucleotide encoding a light chain immunoglobulin amino acid
 CC sequence; (b) inserting the first and second polynucleotide sequences
 CC into a host cell; (c) maintaining the host cell in conditions which allow
 CC the amino acid sequences encoded by the polynucleotides to be expressed
 CC in the host cell; and (d) isolating the antibody comprising the heavy and
 CC light chain immunoglobulin amino acid sequences from the host cell. The
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used for
 CC neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting HIV
 CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and

CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation
 XX
 SQ Sequence 124 AA;
 Query Match 81.8%; Score 649; DB 3; Length 124;
 Best Local Similarity 95.2%; Freq. No. 8.9e-55;
 Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 23 LVQSGAEVKKPGASVKVSQASGYRFSNFVHHVVRQAPGQRFEMWGWINPYNKFSK 82
 Db 1 LEQSGAEVKKPGASVKVSQASGYRFSNFVHHVVRQAPGQRFEMWGWINPYNKFSK 60
 QY 83 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 142
 Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYTWDDSPQDNYMDVWGKTKV 120
 QY 143 IVSS 146
 Db 121 IVSS 124

RESULT 23
 AAY95099
 ID AAY95099 standard; protein; 124 AA.
 XX AC AAY95099;
 XX
 DT 30-JUN-2000 (first entry)
 XX
 DE Anti-gp120 antibody heavy chain variable region from clone b21.
 XX
 KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 XX
 OS Homo sapiens.
 XX
 FN AU9948756-A.
 XX
 PD 17-FEB-2000.
 XX
 PF 16-SEP-1999; 99AU-00048756.
 XX
 PR 16-SEP-1999; 99AU-00048756.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 XX
 DR WPI; 2000-293393/26.
 XX
 PT Novel human monoclonal antibodies which immunoreact with and neutralize
 PT human immunodeficiency virus useful for treating HIV infections.
 XX
 PS Example 9; Fig 10; 366pp; English.
 XX

The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the

CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV
 XX
 SQ Sequence 124 AA;
 Query Match 81.8%; Score 649; DB 3; Length 124;
 Best Local Similarity 95.2%; Pred. No. 8.9e-55;
 Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWRQAPGQRFEMWGWINPYNGNKEFSK 82
 DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWRQAPGQRFEMWGWINPYNGNKEFSK 60
 QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 142
 DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYICARVGPYTWDDSPQDNYMDVWGKGTIV 120
 QY 143 IVSS 146
 DB 121 IVSS 124
 RESULT 24
 AAR75606
 ID AAR75606 standard; protein; 124 AA.
 XX
 AC AAR75606;
 XX
 DT 11-MAR-1996 (first entry)
 DE
 XX VH Fab H4H1-5 binds to gp120.
 XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab;
 KW immunoreaction; neutralisation; passive immunotherapy.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..27
 FT /label= FR1
 FT Region 28..32
 FT /label= CDR1
 FT Region 33..46
 FT /label= FR2
 FT Region 47..63
 FT /label= CDR2
 FT Region 64..95
 FT /label= FR3
 FT Region 96..113
 FT /label= CDR3
 FT Region 114..124
 FT /label= FR4
 XX
 PN WO9511317-A1.
 XX
 PD 27-APR-1995.
 XX
 PF 19-OCT-1994; 94WO-US011907.
 XX
 PR 19-OCT-1993; 93US-00139409.
 PR 26-APR-1994; 94US-00233619.
 PR 19-SEP-1994; 94US-00308841.

XX (SCRI) SCRIPPS RES INST.
 PA Barbas CF, Burton DR, Lerner RA;
 XX
 PI WPI; 1995-170235/22.
 XX
 DR Synthetic human neutralising monoclonal antibodies to human
 XX immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
 PT induced disease.
 PT
 XX Example 4B1; Fig 7; 249pp; English.
 XX
 CC The sequences given in AAR75604-09 represent human Fab's comprising
 CC variable chain heavy regions (VH), which bind to HIV gp120. The six amino
 CC acids which comprise CDR1 have been randomised with 3 of the six CDR1
 CC sequences containing the preferred His residue as the first residue of
 CC CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
 CC used in the production of a human monoclonal antibody (Mab) which is
 CC capable of immunoreacting with, and neutralising HIV. The Mab's are
 CC capable of reducing HIV infectivity titre in an in vitro virus
 CC infectivity assay by 50% at a concentration of <100 ng of antibody per
 CC ml. They can be used to provide passive immunotherapy to HIV in a human.
 CC They neutralise HIV more effectively than antibodies selected from non-
 CC randomised combinatorial libraries
 XX
 SQ Sequence 124 AA;
 Query Match 81.7%; Score 648; DB 2; Length 124;
 Best Local Similarity 96.8%; Pred. No. 1.1e-54;
 Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 23 LVQSGAEVKKPGASVKVSCQASGYRFSNFIHWRQAPGQRFEMWGWINPYNGNKEFSK 82
 DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWRQAPGQRFEMWGWINPYNGNKEFSK 60
 QY 83 FQDRVTFDTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 142
 DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
 QY 143 IVSS 146
 DB 121 IVSS 124
 RESULT 25
 AAR75609
 ID AAR75609 standard; protein; 124 AA.
 XX
 AC AAR75609;
 XX
 DT 11-MAR-1996 (first entry)
 XX
 DE VH Fab H4H1-8 binds to gp120.
 XX
 KW Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab;
 KW immunoreaction; neutralisation; passive immunotherapy.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..27
 FT /label= FR1
 FT Region 28..32
 FT /label= CDR1
 FT Region 33..46
 FT /label= FR2
 FT Region 47..63
 FT /label= CDR2
 FT Region 64..95
 FT /label= FR3
 FT Region 96..113

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FT FT /label= CDR3
FT FT 114..124
FT FT /label= FR4
XX PN WO9511317-A1.
XX PD 27-APR-1995.
XX PF 19-OCT-1994; 94WO-US011907.
XX PR 19-OCT-1993; 93US-00139409.
XX PR 26-APR-1994; 94US-00233619.
XX PR 19-SEP-1994; 94US-00308841.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Burton DR, Lerner RA;
XX PI WPI; 1995-170235/22.
XX PT Synthetic human neutralising monoclonal antibodies to human
XX PT immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
XX PT induced disease.
XX PS Example 4B1; Fig 7; 249pp; English.
XX CC The sequences given in AAR75504-09 represent human Fab's comprising
XX CC variable chain heavy regions (VH), which bind to HIV gp120. The six amino
XX CC acids which comprise CDR1 have been randomised with 3 of the six CDR1
XX CC sequences containing the preferred His residue as the first residue of
XX CC CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
XX CC used in the production of a human monoclonal antibody (MAB) which is
XX CC capable of immunoreacting with, and neutralising HIV. The MAB's are
XX CC capable of reducing HIV infectivity titre in an in vitro virus
XX CC infectivity assay by 50% at a concentration of <100 ng of antibody per
XX CC ml. They can be used to provide passive immunotherapy to HIV in a human.
XX CC They neutralise HIV more effectively than antibodies selected from non-
XX CC randomised combinatorial libraries
XX SQ Sequence 124 AA;

Query Match 81.7%; Score 648; DB 2; Length 124;
Best Local Similarity 96.8%; Pred. No. 1.1e-54;
Matches 120; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSQCASGYRFSNFTVHWVRQAPGQRFWMGWINPYNGNKEFSK 82
DB 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFTVHWVRQAPGQRFWMGWINPYNGNKEFSK 60

QY 83 FQDRVTFADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 142
DB 61 FQDRVTFADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 143 IVSS 146
DB 121 IVSS 124

RESULT 26
AAR75572
ID AAR75572 standard; protein; 124 AA.
XX AC AAR75572;
XX DT 05-MAR-1996 (first entry)
XX DE VH Fab 3b9 binds to gp120.
XX KW Human, Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
XX KW 3b1; 3b3; 3b4; 3b9; M74; humanised; monoclonal antibody; MAB;
XX KW immunoreaction; neutralisation; passive immunotherapy.
XX OS Synthetic.

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```

XX FH Key Location/Qualifiers
XX FT Region 1..27
XX FT /label= FR1
XX FT Region 28..32
XX FT /label= CDR1
XX FT Region 33..46
XX FT /label= FR2
XX FT Region 47..63
XX FT /label= CDR2
XX FT Region 64..95
XX FT /label= FR3
XX FT Region 96..113
XX FT /label= CDR3
XX FT Region 114..124
XX FT /label= FR4
XX PN WO9511317-A1.
XX PD 27-APR-1995.
XX PF 19-OCT-1994; 94WO-US011907.
XX PR 19-OCT-1993; 93US-00139409.
XX PR 26-APR-1994; 94US-00233619.
XX PR 19-SEP-1994; 94US-00308841.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Burton DR, Lerner RA;
XX PI WPI; 1995-170235/22.
XX PT Synthetic human neutralising monoclonal antibodies to human
XX PT immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
XX PT induced disease.
XX PS Claim 6; Page 172-173; 249pp; English.
XX CC The sequences given in AAR75568-72 represent human Fab's comprising
XX CC variable chain heavy regions (VH), which bind to HIV gp120. The Fab's
XX CC 3b1, 3b3, 3b4 and 3b9 have the same amino acid composition as MT4 but
XX CC have randomised amino acids in the entire CDR1 and in four of the 18
XX CC amino acid residues in CDR3. These Fab's are used in the production of a
XX CC human monoclonal antibody (MAB) which is capable of immunoreacting with,
XX CC and neutralising HIV. The MAB's are capable of reducing HIV infectivity
XX CC titre in an in vitro virus infectivity assay by 50% at a concentration of
XX CC <100 ng of antibody per ml. They can be used to provide passive
XX CC immunotherapy to HIV in a human. They neutralise HIV more effectively
XX CC than antibodies selected from non-randomised combinatorial libraries
XX SQ Sequence 124 AA;

Query Match 81.5%; Score 646; DB 2; Length 124;
Best Local Similarity 95.2%; Pred. No. 1.7e-54;
Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 23 LVQSGAEVKKPGASVKVSQCASGYRFSNFTVHWVRQAPGQRFWMGWINPYNGNKEFSK 82
DB 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFTVHWVRQAPGQRFWMGWINPYNGNKEFSK 60

QY 83 FQDRVTFADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 142
DB 61 FQDRVTFADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 143 IVSS 146
DB 121 IVSS 124

RESULT 27
AAR75570
ID AAR75570 standard; protein; 124 AA.

```

XX AAR75570;
 AC 05-MAR-1996 (first entry)
 DT VH Fab 3b3 binds to gp120.
 DE Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 XX 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; MAB;
 KW immunoreaction; neutralisation; passive immunotherapy.
 KW
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1. .27
 FT /label= FR1
 FT Region 28. .32
 FT /label= CDR1
 FT Region 33. .46
 FT /label= FR2
 FT Region 47. .63
 FT /label= CDR2
 FT Region 64. .95
 FT /label= FR3
 FT Region 96. .113
 FT /label= CDR3
 FT Region 114. .124
 FT /label= FR4
 XX WO9511317-A1.
 PN 27-APR-1995.
 PD 19-OCT-1994; 94WO-US011907.
 XX 19-OCT-1993; 93US-00139409.
 PR 26-APR-1994; 94US-00233619.
 PR 19-SEP-1994; 94US-00308841.
 XX (SCRI) SCRIPPS RES INST.
 PA Barbas CF, Burton DR, Lerner RA;
 XX WPI; 1995-170235/22.
 DR Synthetic human neutralising monoclonal antibodies to human
 PT immunodeficiency virus - used for diagnosis and immuno-therapy of HIV-
 PT induced disease.
 XX Claim 6; Page 171; 249pp; English.
 PS The sequences given in AAR75568-72 represent human Fab's comprising
 CC variable chain heavy regions (VH), which bind to HIV gp120. The Fab's
 CC 3b1, 3b3, 3b4 and 3b9 have the same amino acid composition as MT4 but
 CC have randomised amino acids in the entire CDR1 and in four of the 18
 CC amino acid residues in CDR3. These Fab's are used in the production of a
 CC human monoclonal antibody (MAB) which is capable of immunoreacting with,
 CC and neutralising HIV. The MAB's are capable of reducing HIV infectivity
 CC titre in an in vitro virus infectivity assay by 50% at a concentration of
 CC <100 ng of antibody per ml. They can be used to provide passive
 CC immunotherapy to HIV in a human. They neutralise HIV more effectively
 CC than antibodies selected from non-randomised combinatorial libraries
 XX Sequence 124 AA;
 Query Match 81.3%; Score 645; DB 2; Length 124;
 Best Local Similarity 95.2%; Pred. No. 2.2e-54;
 Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 23 LVQSGAEVKKPGASVKVSQCOAGYRFSNFTVHWVRQAPGQRFPEWGMGWINPYNGNKEFSAK 62
 Db 1 LEQSGAEVKKPGASVKVSQCOAGYRFSNFTVHWVRQAPGQRFPEWGMGWINPYNGNKEFSAK 60

QY 83 PQDRVTFPTADTSANTAYMELRSLRSADTAVYICARVGPYSWDDSPQDNYYMDVMGKGTTV 142
 Db 61 PQDRVTFPTADTSANTAYMELRSLRSADTAVYICARVGPYSWDDSPQDNYYMDVMGKGTTV 120
 QY 143 IVSS 146
 Db 121 IVSS 124
 RESULT 28
 AAR54335
 ID AAR54335 standard; protein; 124 AA.
 XX AAR54335;
 AC AAR54335;
 XX 25-MAR-2003 (revised)
 DT 10-NOV-1994 (first entry)
 XX Anti-HIV gp120 immunoglobulin L12-HC12 shuffled heavy chain.
 DE Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; heavy chain; shuffled;
 KW variable region; framework; complementarity determining region.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT Region 1. .31
 FT /label= FR1
 FT Region 32. .36
 FT /label= CDR1
 FT Region 37. .50
 FT /label= FR2
 FT Region 51. .67
 FT /label= CDR2
 FT Region 68. .99
 FT /label= FR3
 FT Region 100. .117
 FT /label= CDR3
 FT Region 118. .124
 FT /label= FR4
 XX WO9407922-A1.
 PN 14-APR-1994.
 PD 30-SEP-1993; 93WO-US009328.
 PF 30-SEP-1992; 92US-00954148.
 PR (SCRI) SCRIPPS RES INST.
 XX Burton DR, Barbas CF, Lerner RA;
 XX WPI; 1994-135516/16.
 DR New human monoclonal antibodies neutralising HIV - react with gp120 or
 PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
 PT diagnosis and for passive immuno-therapy.
 XX Example; Page 206-207; 248pp; English.
 PS The anti-HIV gp120 light chain clone b12 (AAR54253) was recombined with a
 CC heavy chain library to construct a new library L12-HCN. Ten heavy chains
 CC which recombined with the b12 light chain and bound gp120 by panning were
 CC chosen for sequence analysis. AAR54335 was one of these heavy chains.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 124 AA;
 Query Match 80.9%; Score 641.5; DB 2; Length 124;
 Best Local Similarity 94.4%; Pred. No. 4.7e-54;
 Matches 117; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 20 QVQLV-OSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGMWNPYNGNKE 78
 DB 1 QVQLLEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGMWNPYNGNKE 60
 QY 79 FSAKFQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGK 138
 DB 61 FSAKFRDRVTFTADTDANTAYMELRSLSADTAIYYCARVGPYTWDDSPQDNYMDVWGK 120
 QY 139 GTTV 142
 DB 121 GTTV 124

RESULT 29
 AAW01309
 ID AAW01309 standard; protein; 124 AA.
 AC AAW01309;
 XX 29-JAN-1997 (first entry)
 DT VH region of HIV neutralising Mab, clone HC12.
 XX Heavy chain; light chain; variable region; VH; monoclonal antibody; Mab;
 KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Region 1..31
 FT /label= FR1
 FT Region 32..36
 FT /label= CDR1
 FT Region 37..50
 FT /label= FR2
 FT Region 51..67
 FT /label= CDR2
 FT Region 68..99
 FT /label= FR3
 FT Region 100..117
 FT /label= CDR3
 FT Region 118..124
 FT /label= FR4
 XX
 DN W09602273-A1.
 XX
 XX 01-FEB-1996.
 XX
 XX 11-JUL-1995; 95WO-US008743.
 XX
 XX 18-JUL-1994; 94US-00276952.
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA Burton DR, Barbas CF, Lerner RA;
 PI WPI; 1996-179601/18.
 XX
 XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
 PT immuno:therapy and detection of HIV infection.
 XX
 XX Example; Fig 13; 366pp; English.
 PS
 CC The sequences given in AAW01302-11 represent the heavy chain variable
 CC regions (VH) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the gene
 CC clone, HC12. These sequences represent heavy chains which bind to the b12
 CC light chain clone (see also AAW01276). These sequences were isolated from
 CC the shuffled heavy chain library, Hn-112. A Mab containing this VH

CC sequence has the capacity to reduce HIV infectivity titre in an in vivo
 CC virus infectivity assay by 50 % at a concentration of less than 700 ng of
 CC antibody/ml, and binds mature gp120 preferentially over the precursor
 CC gp160. The Mab may be used for determining immunocompetence of a human
 CC anti-HIV antibody and in the detection of HIV infection. The heavy chain
 CC clones designated H2 and H14 exhibited approx. 40 % neutralisation of HIV
 CC in a syncytia assay
 XX
 SQ Sequence 124 AA;
 Query Match 80.9%; Score 641.5; DB 2; Length 124;
 Best Local Similarity 94.4%; Pred. No. 4.7e-54;
 Matches 117; Conservative 5; Mismatches 1; Indels 1; Gaps 1;
 QY 20 QVQLV-OSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGMWNPYNGNKE 78
 DB 1 QVQLLEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGMWNPYNGNKE 60
 QY 79 FSAKFQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGK 138
 DB 61 FSAKFRDRVTFTADTDANTAYMELRSLSADTAIYYCARVGPYTWDDSPQDNYMDVWGK 120
 QY 139 GTTV 142
 DB 121 GTTV 124

RESULT 30
 AAY98270
 ID AAY98270 standard; protein; 124 AA.
 XX AAY98270;
 AC AAY98270;
 DT 04-JUL-2000 (first entry)
 DE Anti-gp120 HC12 heavy chain variable amino acid sequence.
 KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX Homo sapiens.
 OS AU9948754-A.
 PN 17-FEB-2000.
 PD
 XX 16-SEP-1999; 99AU-00048754.
 PF 16-SEP-1999; 99AU-00048754.
 PR (SCRI) SCRIPPS RES INST.
 PA Burton DR, Barbas CF, Lerner RA;
 PI WPI; 2000-246867/22.
 XX
 XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
 PT (HIV) used for providing passive immunotherapy to HIV are specific for
 PT glycoprotein-120.
 XX
 XX Example 9; Fig 13; 374pp; English.
 PS
 CC This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity
 CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
 CC production of the antibody comprises: (a) providing a first
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 CC (which does not comprise the sequence represented by AAY98206) and a
 CC second polynucleotide encoding a light chain immunoglobulin amino acid

CC sequence; (b) inserting the first and second polynucleotide sequences
CC into a host cell; (c) maintaining the host cell in conditions which allow
CC the amino acid sequences encoded by the polynucleotides to be expressed
CC in the host cell; and (d) isolating the antibody comprising the heavy and
CC light chain immunoglobulin amino acid sequences from the host cell. The
CC anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used for
CC neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting HIV
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the antibodies
CC associated with monoclonal antibodies of xenogeneic or chimeric
CC derivation
XX
SQ Sequence 124 AA;
Query Match 80.9%; Score 641.5; DB 3; Length 124;
Best Local Similarity 94.4%; Pred. No. 4.7e-54;
Matches 117; Conservative 5; Mismatches 1; Indels 1; Gaps 1;
QY 20 QVQLV-CSGAEVKKPGASVKVSQCSGYRFSNFIHWVRQAPGQRFPEWNGWINPYNGNKE 78
Db 1 QVKLEQSGAEVKKPGASVKVSQCSGYRFSNFIHWVRQAPGQRFPEWNGWINPYNGNKE 50
QY 79 FSAKFQDRVTFTADTSANTAYMELSLRSADTAIYYCARVGPYSWDDSPQDNYIMDVWGK 138
Db 61 FSAKPRDVTFTADTDANTAYMELSLRSADTAIYYCARVGPYTWDDSPQDNYIMDVWGK 120
QY 139 GTTV 142
Db 121 GTTV 124

Search completed: August 26, 2004, 13:37:45
Job time : 56.5333 secs

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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:32:07 ; Search time 45.4667 Seconds
(without alignments)
770.584 Million cell updates/sec

Title: US-10-016-986-66
Perfect score: 674
Sequence: 1 LEQSGAEVKPGASVKVSCO.....PDQNYMDVWGKTTIVVSS 124

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	674	100.0	124	2	AAR54244 Anti-HIV
2	674	100.0	124	2	AAR75568 VH Fab MT
3	674	100.0	124	2	AAW01227 VH region
4	674	100.0	124	3	AAAY98206
5	674	100.0	124	3	AAAY95097
6	667	99.0	146	2	AAW01228
7	667	99.0	146	3	AAAY98285
8	667	99.0	146	3	AAAY95176
9	667	99.0	146	7	ADDE6734
10	667	99.0	146	7	ABRG1564
11	664	98.5	124	2	AAAR75604
12	663	98.4	124	2	AAAR75605
13	660	97.9	124	2	AAAR54245
14	660	97.9	124	3	AAAY98207
15	660	97.9	124	3	AAAY95098
16	660	97.9	124	3	AAAY95098
17	657	97.5	124	2	AAAR75607
18	657	97.5	124	2	AAAR75608
19	656	97.3	124	2	AAAR54246
20	656	97.3	124	2	AAW01247
21	656	97.3	124	3	AAAY98208
22	656	97.3	124	3	AAAY95099
23	655	97.2	124	2	AAAR75606
24	655	97.2	124	2	AAAR75609
25	653	96.9	124	2	AAAR75572

26	652	96.7	124	2	AAR75570
27	652	96.7	250	3	AAAY44346
28	646	95.8	124	2	AAR54335
29	646	95.8	124	2	AAW01309
30	646	95.8	124	3	AAAY98270
31	646	95.8	124	3	AAAY95161
32	642	95.3	124	2	AAR75569
33	629.5	93.4	123	2	AAR75571
34	636	92.9	124	2	AAR75617
35	636	92.9	124	2	AAR75616
36	625	92.7	124	2	AAAR75615
37	619	91.8	124	2	AAAR75610
38	619	91.8	124	2	AAAR75613
39	618	91.7	124	2	AAAR75611
40	617	91.5	124	2	AAAR75612
41	617	91.5	124	2	AAAR75614
42	607	90.1	124	2	AAAR75640
43	606	89.9	124	2	AAAR75638
44	606	89.9	124	2	AAAR75641
45	605	89.8	124	2	AAAR75639
46	577	85.6	124	2	AAAR54331
47	577	85.6	124	2	AAW01305
48	577	85.6	124	3	AAAY98266
49	577	85.6	124	3	AAAY95157
50	554	82.2	124	2	AAAR54330
51	554	82.2	124	2	AAAR54336
52	554	82.2	124	2	AAW01310
53	554	82.2	124	2	AAW01304
54	554	82.2	124	3	AAAY98271
55	554	82.2	124	3	AAAY98265
56	554	82.2	124	3	AAAY95156
57	554	82.2	124	3	AAAY95162
58	548	81.3	125	2	AAAR54333
59	548	81.3	125	2	AAAR54268
60	548	81.3	125	2	AAW01307
61	548	81.3	125	2	AAW01303
62	548	81.3	125	3	AAAY98264
63	548	81.3	125	3	AAAY98264
64	548	81.3	125	3	AAAY95159
65	548	81.3	125	3	AAAY95155
66	545	80.9	124	2	AAAR54332
67	545	80.9	124	2	AAAY98267
68	545	80.9	124	3	AAAY98267
69	541	80.3	126	3	AAAY95158
70	541	80.3	126	3	AAAY95158
71	541	80.3	126	3	AAAY98263
72	541	80.3	126	3	AAAY95154
73	538	79.8	124	2	AAAR54269
74	538	79.8	124	2	AAW01311
75	538	79.8	124	3	AAAY98272
76	538	79.8	124	3	AAAY95163
77	538	79.8	126	2	AAW01302
78	527	78.2	125	2	AAAR54334
79	527	78.2	125	2	AAW01308
80	527	78.2	125	3	AAAY98269
81	527	78.2	125	3	AAAY95160
82	455.5	67.6	253	5	ABP45848
83	454.5	67.4	245	5	ABP45885
84	452.5	67.1	253	5	ABP45519
85	449.5	66.7	230	4	AAU08382
86	449.5	66.7	230	4	AAU08383
87	446.5	66.2	249	5	ABP45719
88	444	65.9	251	5	ABP45066
89	444	65.9	257	5	ABP45343
90	443	65.7	124	6	AAE37618
91	442	65.6	127	6	ADA89122
92	440.5	65.4	123	5	AAO18448
93	440.5	65.4	139	2	AAAR43689
94	440.5	65.4	139	2	AAAR62678
95	440.5	65.4	139	2	AAAR62679
96	440	65.3	255	5	ABP45179
97	438	65.0	123	6	ABR55795
98	438	65.0	251	5	ABP44949

99 438 65.0 252 5 ABP45943
100 437.5 64.9 251 5 ABP45910

Abp45943 Human Bly
Abp45910 Human Bly

ALIGNMENTS

RESULT 1
AAR54244

ID AAR54244 standard; protein; 124 AA.

XX AAR54244;
AC AAR54244;

25-MAR-2003 (revised)
10-NOV-1994 (first entry)

XX Anti-HIV gp120 immunoglobulin heavy chain variable region b4.

XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; heavy chain; variable region;
KW framework region; complementarity determining region.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..27
FT /label= FR1
FT Region 28..32
FT /label= CDR1
FT Region 33..46
FT /label= FR2
FT Region 47..63
FT /label= CDR2
FT Region 64..95
FT /label= FR3
FT Region 96..113
FT /label= CDR3
FT Region 114..124
FT /label= FR4

XX WO9407922-A1.

XX 14-APR-1994.

XX 30-SEP-1993; 93WO-US009328.

XX 30-SEP-1992; 92US-00954148.

XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;

XX WPI; 1994-135516/16.

XX New human monoclonal antibodies neutralising HIV - react with gp120 or
PT gp120 and nucleic acid encoding them, useful for in vivo or in vitro
PT diagnosis and for passive immuno-therapy.

XX Claim 1; Page 163-164; 248pp; English.

XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
CC using primers specific for heavy and light chain variable regions. The
CC amplification products were inserted into a dicistronic vector to produce
CC a library of fragments. E.coli Xli Blue cells were transformed with the
CC library. Filamentous phage were produced which expressed the VAB regions
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC immunoreactive clones. The heavy chain VH region sequence AAR54244
XX neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 124 AA;

Query Match 100.0%; Score 674; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.9e-61;

Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFVTHWVRQAPGQRFEMWGWINPYNNGKFSAK 60
DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFVTHWVRQAPGQRFEMWGWINPYNNGKFSAK 60
QY 61 FQDRVTFTADTSANTAYMELRSLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 61 FQDRVTFTADTSANTAYMELRSLSADTAVYCARVGPYSWDDSPQDNYMDVWGKTTV 120
QY 121 IVSS 124
DB 121 IVSS 124

RESULT 2

AAR75568

ID AAR75568 standard; protein; 124 AA.

XX AAR75568;

DT 05-MAR-1996 (first entry)

DE VH Fab MT4 binds to gp120.

XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab;
KW immunoreaction; neutralisation; passive immunotherapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..27
FT /label= FR1
FT Region 28..32
FT /label= CDR1
FT Region 33..46
FT /label= FR2
FT Region 47..63
FT /label= CDR2
FT Region 64..95
FT /label= FR3
FT Region 96..113
FT /label= CDR3
FT Region 114..124
FT /label= FR4

XX WO9511317-A1.

XX 27-APR-1995;

XX 19-OCT-1994; 94WO-US011907.

XX 19-OCT-1993; 93US-00139409.

XX 26-APR-1994; 94US-00233619.

XX 19-SEP-1994; 94US-00308841.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Burton DR, Lerner RA;

XX WPI; 1995-170235/22.

XX N-PSDB; AAQ92540.

XX Synthetic human neutralising monoclonal antibodies to human
PT immunodeficiency virus - used for diagnosis and immuno-therapy of HIV-
PT induced disease.

XX Claim 9; Page 170; 249pp; English.

XX The sequences given in AAR75568-72 represent human Fab's comprising
CC variable chain heavy regions (VH), which bind to HIV gp120. The Fab's
CC 3b1, 3b3, 3b4 and 3b9 have the same amino acid composition as Mt4 but

CC have randomised amino acids in the entire CDR1 and in four of the 18
 CC amino acid residues in CDR3. These Fab's are used in the production of a
 CC human monoclonal antibody (Mab) which is capable of immunoreacting with,
 CC and neutralising HIV. The Mab's are capable of reducing HIV infectivity
 CC titre in an in vitro virus infectivity assay by 50% at a concentration of
 CC <100 ng of antibody per ml. They can be used to provide passive
 CC immunotherapy to HIV in a human. They neutralise HIV more effectively
 CC than antibodies selected from non-randomised combinatorial libraries
 XX
 SQ Sequence 124 AA;

Query Match 100.0%; Score 674; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 7.9e-61;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKKEFSK 60
 DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKKEFSK 60
 QY 61 FQDRVTFDTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
 DB 61 FQDRVTFDTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
 QY 121 IVSS 124
 DB 121 IVSS 124

RESULT 3
 AAW01227
 ID AAW01227 standard; protein; 124 AA.

XX AC AAW01227;
 XX
 DT 27-JAN-1997 (first entry)
 XX DE VH region of HIV neutralising Mab, clones b4 and b12.
 XX
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody; Mab;
 KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 1..27
 FT /label= FR1
 FT Region 28..32
 FT /label= CDR1
 FT Region 33..46
 FT /label= FR2
 FT Region 47..63
 FT /label= CDR2
 FT Region 64..95
 FT /label= FR3
 FT Region 96..113
 FT /label= CDR3
 FT Region 114..124
 FT /label= FR4

XX WO9602273-A1.

XX 01-FEB-1996.

XX 11-JUL-1995; 95WO-US008743.

XX 18-JUL-1994; 94US-00276952.

XX (SCRI) SCRIPPS RES INST.

XX PA Burton DR, Barbas CF, Lerner RA;

XX

DR WPI; 1996-179601/18.

XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
 PT immuno:therapy and detection of HIV infection.

XX Claim 9; Fig 10; 366pp; English.

XX This sequence represents the heavy chain variable region (VH) of a
 CC monoclonal antibody (Mab) which is immunoreactive with HIV glycoprotein
 CC gp120 and is capable of neutralising HIV. This sequence represents the
 CC sequence of clones b4 and b12. The Mab has the capacity to reduce HIV
 CC infectivity titre in an in vivo virus infectivity assay by 50% at a
 CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
 CC preferentially over the precursor gp160. This sequence forms the heavy
 CC chain component of Mab's with the light chain sequences given in
 CC AAW01273, AAW01275-76, AAW01293, AAW01296, and AAW01299-300. The Mab may
 CC be used for determining immunocompetence of a human anti-HIV antibody and
 CC in the detection of HIV infection

SQ Sequence 124 AA;

Query Match 100.0%; Score 674; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 7.9e-61;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKKEFSK 60
 DB 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGKKEFSK 60
 QY 61 FQDRVTFDTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
 DB 61 FQDRVTFDTADTSANTAYMELRSLSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
 QY 121 IVSS 124
 DB 121 IVSS 124

RESULT 4

AA98206

ID AA98206 standard; protein; 124 AA.

XX AC AA98206;

XX 04-JUL-2000 (first entry)

DE Anti-Gp120 antibody heavy chain variable region from clone b4.

XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.

XX OS Homo sapiens.

XX PN AU9948754-A.

XX 17-FEB-2000.

XX 16-SEP-1999; 99AU-00048754.

XX 16-SEP-1999; 99AU-00048754.

XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;

XX WPI; 2000-246867/22.

XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
 PT (HIV) used for providing passive immunotherapy to HIV are specific for
 PT glycoprotein-120.

XX

Claim 1; Fig 10; 374pp; English.

This sequence represents a fragment of the antibodies of the invention. The invention relates to the production of an anti-HIV (human immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable of reducing an HIV infectivity titre in an in vitro virus infectivity assay by 50% at a concentration of less than 70 ng/ml. The method for the production of the antibody comprises: (a) providing a first polynucleotide encoding a heavy chain immunoglobulin amino acid sequence (which does not comprise the sequence represented by AAY98206) and a second polynucleotide encoding a light chain immunoglobulin amino acid sequence; (b) inserting the first and second polynucleotide sequences into a host cell; (c) maintaining the host cell in conditions which allow the amino acid sequences encoded by the polynucleotides to be expressed in the host cell; and (d) isolating the antibody comprising the heavy and light chain immunoglobulin amino acid sequences from the host cell. The anti-HIV gp-120 monoclonal antibody is used for providing passive immunotherapy to HIV in a human. They can be administered to high-risk patients to reduce the likelihood and/or severity of HIV-induced disease and to patients who are already HIV-infected. The antibodies are used for neutralising field isolates which provides information about the immunocompetence of an immune response in HIV patients, for detecting HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for producing anti-idiotypic antibodies which can be used for active immunisation and to screen human monoclonal antibodies to identify those with the same binding specificity and to monitor the course of HIV disease therapy by measuring the changes in concentration of HIV present in the body or in body fluids by immunoassay. The anti-HIV gp-120 monoclonal antibodies are encoded by a human polynucleotide sequence and when used in vivo for diagnosis and immunotherapy of HIV-induced disease reduce the problems of significant host immune response to the antibodies associated with monoclonal antibodies of xenogenic or chimeric derivation. Note: The present sequence is specifically not claimed

Sequence 124 AA;

Query Match 100.0%; Score 674; DB 3; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.9e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGKFSK 60
DB 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGKFSK 60

QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 121 IVSS 124
DB 121 IVSS 124

RESULT 5

AA95097
ID AAY95097 standard; protein; 124 AA.

AC AAY95097;

DT 30-JUN-2000 (first entry)

DE Anti-gp120 antibody heavy chain variable region from clone b4.

XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
XX reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
XX glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.

OS Homo sapiens.

XX AU9948756-A.

XX 17-FEB-2000.

PD

XX

PF 16-SEP-1999; 99AU-00048756.
XX
PR 16-SEP-1999; 99AU-00048756.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 2000-293393/26.
DR
XX Novel human monoclonal antibodies which immunoreact with and neutralize
PT human immunodeficiency virus useful for treating HIV infections.
XX
XX Example 9; Fig 10; 366pp; English.

The present sequence represents a fragment of an anti-human immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV mature glycoprotein gp120 preferentially over HIV precursor glycoprotein gp160 and neutralises HIV and which reduces HIV infectivity titre in an in vitro virus infectivity assay by 50% at a concentration of less than 700 ng/ml. The antibodies are used as reagents for the diagnosis and immunotherapy of HIV induced disease. They are useful as neutralising field isolates and provide useful information regarding the immunocompetence of an immune response in HIV infected patients. The monoclonal antibodies are useful for producing anti-idiotypic antibodies which can be used to screen human monoclonal antibodies to identify whether the antibody has the same binding specificity as the antibodies of the invention. The neutralising antibodies define new epitopes on the HIV gp120 and gp41 glycoproteins, thus increasing the availability of new immunotherapeutic human monoclonal antibodies. A major advantage of the monoclonal antibodies derives from the fact that they are encoded by a human polynucleotide sequence. Thus in vivo use of the monoclonal antibodies for diagnosis and immunotherapy of HIV induced disease greatly reduces the problems of significant host immune response to the passively administered antibodies which is a problem commonly encountered when monoclonal antibodies of xenogenic or chimeric derivation are utilized. An additional major advantage of the monoclonal antibodies described derives from the fact that they immunoreact with a unique determinant present on mature HIV glycoprotein gp120. This class of antibodies is particularly effective at neutralising field isolates of HIV

Sequence 124 AA;

Query Match 100.0%; Score 674; DB 3; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.9e-61;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGKFSK 60
DB 1 LEQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGKFSK 60

QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120
DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKTTV 120

QY 121 IVSS 124
DB 121 IVSS 124

RESULT 6

AAW01228
ID AAW01228 standard; protein; 146 AA.

XX AAW01228;

XX 16-OCT-2003 (revised)

DT 27-JAN-1997 (first entry)

XX VH region of HIV neutralising Mab, IgG1 b12.

XX Heavy chain; light chain; variable region; VH; monoclonal antibody; Mab;

KW

KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 XX
 OS Homo sapiens.
 OS Mus musculus.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "Mouse B72.3 heavy chain leader sequence"
 FT Peptide 21..26
 FT /note= "Human VH consensus sequence"
 FT Protein 27..146
 FT /note= "Human Fab b12"
 XX
 PN WO9602273-A1.
 XX
 XX 01-FEB-1996.
 XX
 XX 11-JUL-1995; 95WO-US008743.
 XX
 XX 18-JUL-1994; 94US-00276852.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Burton DR, Barbas CF, Lerner RA;
 XX
 XX WPI; 1996-179601/18.
 DR N-PSDB; AAT40914.
 XX
 XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
 XX immuno:therapy and detection of HIV infection.
 XX
 XX Claim 10; Page 275-276; 366pp; English.
 XX
 XX This sequence represents the heavy chain variable region (VH) of a
 CC monoclonal antibody (Mab) which is immunoreactive with HIV glycoprotein
 CC gp120 and is capable of neutralising HIV. This sequence contains the
 CC leader sequence derived from the mouse B72.3 heavy chain, and the human
 CC VH consensus sequence attached to the N-terminal of the b12 VH sequence.
 CC The DNA sequence contains a Kozak sequence for the control of VH
 CC expression. This sequence was amplified using the primer sequences given
 CC in AAT40889-92. A Mab containing this VH sequence has the capacity to
 CC reduce HIV infectivity titre in an in vivo virus infectivity assay by 50
 CC % at a concentration of less than 700 ng of antibody/ml, and binds mature
 CC gp120 preferentially over the precursor gp160. The Mab may be used for
 CC determining immunocompetence of a human anti-HIV antibody and in the
 CC detection of HIV infection. (Updated on 16-OCT-2003 to standardise OS
 CC field)
 XX
 XX Sequence 146 AA;
 SQ
 Query Match 99.0%; Score 667; DB 2; Length 146;
 Best Local Similarity 99.2%; Pred. No. 4.9e-60;
 Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEFSK 60
 DB 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEFSK 82
 QY 61 FQDRVTFTADTSANTAYMELRSLSADTAVYICARVPYSWDDSPQDNYMDVWGKGTIV 120
 DB 83 FQDRVTFTADTSANTAYMELRSLSADTAVYICARVPYSWDDSPQDNYMDVWGKGTIV 142
 QY 121 IVSS 124
 DB 143 IVSS 146
 RESULT 7
 AAY98285
 ID AAY98285 standard; protein; 146 AA.

XX
 AC AAY98285;
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Modified heavy chain variable region amino acid sequence.
 XX
 KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX
 OS Synthetic.
 XX
 PN AU9948754-A.
 XX
 XX 17-FEB-2000.
 PD
 XX 16-SEP-1999; 99AU-00048754.
 PF
 XX 16-SEP-1999; 99AU-00048754.
 PR
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Burton DR, Barbas CF, Lerner RA;
 PI
 XX WPI; 2000-246867/22.
 DR
 XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
 PT (HIV) used for providing passive immunotherapy to HIV are specific for
 PT glycoprotein-120.
 PT
 XX Example 4; Page 275-276; 374pp; English.
 PS
 XX This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity
 CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
 CC production of the antibody comprises: (a) providing a first
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 CC (which does not comprise the sequence represented by AAY98206) and a
 CC second polynucleotide encoding a light chain immunoglobulin amino acid
 CC sequence; (b) inserting the first and second polynucleotide sequences
 CC into a host cell; (c) maintaining the host cell in conditions which allow
 CC the amino acid sequences encoded by the polynucleotides to be expressed
 CC in the host cell; and (d) isolating the antibody comprising the heavy and
 CC light chain immunoglobulin amino acid sequences from the host cell. The
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used for
 CC neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting HIV
 CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation
 XX
 SQ Sequence 146 AA;
 Query Match 99.0%; Score 667; DB 3; Length 146;
 Best Local Similarity 99.2%; Pred. No. 4.9e-60;
 Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEFSK 60

Db 23 LVQSGAEVKPGASVKVSCQASGYRFSNFIHVWRQAPGQRFEMWGWINPYNKGKFSAX 82
 QY 61 FQDRVTFADTSANTAYMELRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKGTIV 120
 Db 83 FQDRVTFADTSANTAYMELRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKGTIV 142
 QY 121 IVSS 124
 Db 143 IVSS 146
 RESULT 8
 ID AAY95176 standard; protein; 146 AA.
 AC AAY95176;
 DT 30-JUN-2000 (first entry)
 DE Modified heavy chain variable region amino acid sequence.
 KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 OS Synthetic.
 PN AU9948756-A.
 PD 17-FEB-2000.
 PF 16-SEP-1999; 99AU-00048756.
 PR 16-SEP-1999; 99AU-00048756.
 PA (SCRI) SCRIPPS RES INST.
 PI Burton DR, Barbas CF, Lerner RA;
 XX WPI; 2000-293393/26.
 DR Novel human monoclonal antibodies which immunoreact with and neutralize
 PT human immunodeficiency virus useful for treating HIV infections.
 PS Example 4; Page 111; 366pp; English.
 CC The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50% at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of the
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV

XX Sequence 146 AA;
 QY Query Match 99.0%; Score 667; DB 3; Length 146;
 Db Best Local Similarity 99.2%; Pred. No. 4.9e-60;
 QY Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHVWRQAPGQRFEMWGWINPYNKGKFSAX 60
 QY 23 LVQSGAEVKPGASVKVSCQASGYRFSNFIHVWRQAPGQRFEMWGWINPYNKGKFSAX 82
 Db 61 FQDRVTFADTSANTAYMELRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKGTIV 120
 QY 83 FQDRVTFADTSANTAYMELRSADTAVYVCARVGPYSWDDSPQDNYMDVWGKGTIV 142
 Db 121 IVSS 124
 Db 143 IVSS 146
 RESULT 9
 ID ADE06734 standard; protein; 146 AA.
 AC ADE06734;
 DT 29-JAN-2004 (first entry)
 DE Human IgG Fab b12 heavy chain protein SEQ ID NO:4.
 KW hybrid polypeptide; protein aggregation; prion polypeptide;
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant;
 KW cerebrotective; antiparkinsonian; cytosatic; nephrotropic; cardiant;
 KW antiinflammatory; antiarteriosclerotic; gene therapy;
 KW Creutzfeldt-Jakob disease; scrapie and bovine spongiform encephalopathy;
 KW Alzheimer's disease; Type II diabetes; Huntington's disease;
 KW immunoglobulin amyloidosis; amyloidosis; chronic inflammatory disease;
 KW amyotrophic lateral sclerosis; Pick's disease; Parkinson's disease;
 KW Frontotemporal dementia; multiple myeloma; plasma cell dyscrasia;
 KW familial amyloidotic polyneuropathy; medullary carcinoma;
 KW chronic renal failure; congestive heart failure; chronic inflammation;
 KW atherosclerosis; human.
 OS Homo sapiens.
 PN WC2003085086-A2.
 PD 16-OCT-2003.
 PF 08-APR-2003; 2003WO-US010856.
 PR 09-APR-2002; 2002US-0371610P.
 PA (SCRI) SCRIPPS RES INST.
 PI Burton DR, Williamson RA, Moroncini G;
 XX WPI; 2003-877028/81.
 DR N-PSDB; ADE06733.
 CC New motif-grafted hybrid polypeptides binding to the infectious form of a
 CC prion, useful for diagnosing or treating diseases of protein aggregation
 CC or conformation, e.g. amyloidosis, Alzheimer's disease, renal failure or
 CC diabetes.
 CC Claim 37; SEQ ID NO 4; 115pp; English.
 CC The present invention describes a hybrid polypeptide (I) comprising: (a)
 CC a polypeptide motif containing a sufficient number of contiguous amino
 CC acid residues from a polypeptide associated with a disease of protein
 CC aggregation or conformation to bind an aggregating form of the
 CC polypeptide or to a disease-associated conformer of the polypeptide; and
 CC (b) an additional amino acids from a polypeptide other than the

polypeptide from which the motif is derived, where the resulting hybrid polypeptide binds with greater affinity to a disease causing or infectious conformer of the polypeptide that is the source of the polypeptide motif compared to a benign form of the polypeptide. Also described: (1) a nucleic acid molecule encoding (1); (2) a vector comprising the nucleic acid molecule; (3) a cell comprising the vector; (4) detecting an isoform or a prpsc form of a prion polypeptide or a polypeptide associated with a disease of protein aggregation, in a sample; (5) a solid support comprising a plurality of polypeptides described above; (6) detecting cells that contain a protein conformer associated with a disease of protein aggregation; (7) preparing a hybrid molecule that specifically interacts with one conformer of a protein involved in the disease mentioned above; and (8) an anti-idiotypic antibody that specifically binds to an infectious form of a prion protein. (I) has neuroprotective, neurotropic, antidiabetic, anticonvulsant, cerebroprotective, antiparkinsonian, cytostatic, neurotropic, cardiant, antiinflammatory and antiarteriosclerotic activities, and can be used in gene therapy. The composition and methods of the present invention can be used in diagnosing or treating diseases of protein aggregation or conformation, such as Creutzfeldt-Jakob disease, scrapie and bovine spongiform encephalopathy, Alzheimer's disease, Type II diabetes, Huntington's disease, immunoglobulin amyloidosis, reactive amyloidosis associated with chronic inflammatory disease, hereditary systemic amyloidosis associated with autosomal dominant inheritance of variant transthyretin gene, amyotrophic lateral sclerosis, Pick's disease, Parkinson's disease, frontotemporal dementia, multiple myeloma, plasma cell dyscrasias, familial amyloidotic polyneuropathy, medullary carcinoma of thyroid, chronic renal failure, congestive heart failure, senile cardiac and systemic amyloidosis, chronic inflammation, atherosclerosis or familial amyloidosis. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 146 AA;

Query Match 99.0%; Score 667; DB 7; Length 146;
Best Local Similarity 99.2%; Pred. No. 4.9e-60;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGMINPYNGNKEFSK 60
DB 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGMINPYNGNKEFSK 82
QY 61 FQDRVTFADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 83 FQDRVTFADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 142
QY 121 IVSS 124
DB 143 IVSS 146

RESULT 10
ABR61564
ID ABR61564 standard; protein; 476 AA.

XX ABR61564;
XX
XX 15-JAN-2004 (first entry)
XX Human MAb IgG1b12 heavy chain.
XX Adeno-associated virus; rAAV; IgG1b12; ScFvX5; anti-HIV; antibacterial;
XX antirheumatic; antiarthritic; cytostatic; sedative; antiinflammatory;
XX neuroprotective; gene therapy; vaccine; antibody; Mab.
XX Homo sapiens.
XX
XX WO2003087324-A2.
XX
XX 23-OCT-2003.
XX
XX 09-APR-2003; 2003WO-US010865.

PR 09-APR-2002; 2002US-0371501P.
XX (CHIL-) CHILDRENS HOSPITAL INC.
XX

XX Clark KR, Johnson PR;
XX
XX WPI; 2003-833721/77.
XX N-PSDB; ACF58045.

XX New recombinant adeno-associated virus (rAAV)/IgG1b12 or rAAV/ScFvX5
XX genome, useful for preventing or treating viral infections (e.g. HIV),
XX bacterial infections or other chronic disease states (e.g. cancer,
XX inflammation or kuru).

XX Example 1; Page 35-37; Opp; English.

XX The invention relates to a recombinant adeno-associated virus (rAAV)/
XX IgG1b12 or rAAV/ScFvX5 genome. The rAAV is useful for gene delivery,
XX particularly in delivering antibody genes to target cells in mammals. The
XX antibodies may be used to prevent and/or treat viral infections
XX (particularly HIV), bacterial infections and other chronic disease states
XX (e.g. cancer, rheumatoid arthritis, inflammation, fatal familial
XX insomnia, kuru, Mad Cow Disease or Alpers syndrome). The present sequence
XX represents the human monoclonal antibody (Mab) IgG1b12 heavy chain
XX

XX SQ Sequence 476 AA;

Query Match 99.0%; Score 667; DB 7; Length 476;
Best Local Similarity 99.2%; Pred. No. 1.9e-59;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGMINPYNGNKEFSK 60
DB 23 LVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGMINPYNGNKEFSK 82
QY 61 FQDRVTFADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 83 FQDRVTFADTSANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGTIV 142
QY 121 IVSS 124
DB 143 IVSS 146

RESULT 11
AAR75604
ID AAR75604 standard; protein; 124 AA.

XX AAR75604;
XX
XX 11-MAR-1996 (first entry)
XX VH Fab H4H1-1 binds to gp120.
XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
XX 3b1, 3b3; 3b4; MT4; humanised; monoclonal antibody; Mab;
XX immunoreaction; neutralisation; passive immunotherapy.

XX Synthetic.

XX Key Location/Qualifiers
XX Region 1..27
XX /label= FR1
XX Region 28..32
XX /label= CDR1
XX Region 33..46
XX /label= FR2
XX Region 47..63
XX /label= CDR2
XX Region 64..95
XX /label= FR3
XX Region 96..113
XX /label= CDR3

Thu Aug 26 14:28:11 2004

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FT Region 114..124
FT /label= FR4
XX WO9511317-A1.
XX 27-APR-1995.
XX 19-OCT-1994; 94WO-US011907.
XX 19-OCT-1993; 93US-00139409.
XX 26-APR-1994; 94US-00233619.
XX 19-SEP-1994; 94US-00308841.
XX (SCRI ) SCRIPPS RES INST.
XX Barbas CF, Burton DR, Lerner RA;
XX WPI; 1995-170235/22.
XX Synthetic human neutralising monoclonal antibodies to human
XX immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
XX induced disease.
XX Example 4B1; Fig 7; 249pp; English.
XX The sequences given in AAR75604-09 represent human Fab's comprising
XX variable chain heavy regions (VH), which bind to HIV gp120. The six amino
XX acids which comprise CDR1 have been randomised with 3 of the six CDR1
XX sequences containing the preferred His residue as the first residue of
XX CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
XX capable of immunoreacting with, and neutralising HIV. The Mab's are
XX capable of reducing HIV infectivity titre in an in vitro virus
XX infectivity assay by 50% at a concentration of <100 ng of antibody per
XX ml. They can be used to provide passive immunotherapy to HIV in a human.
XX They neutralise HIV more effectively than antibodies selected from non-
XX randomised combinatorial libraries
XX Sequence 124 AA;
XX Query Match 98.5%; Score 664; DB 2; Length 124;
XX Best Local Similarity 97.6%; Pred. No. 8.2e-60;
XX Matches 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGNKEFSAX 60
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGNKEFSAX 60
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYNDVWGKGTIV 120
DB 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYNDVWGKGTIV 120
QY 121 IVSS 124
DB 121 IVSS 124
RESULT 12
AAR75605
ID AAR75605 standard; protein; 124 AA.
XX AAR75605;
XX 11-MAR-1996 (first entry)
XX VH Fab H4H1-3 binds to gp120.
XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
XX 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab;
XX immunoreaction; neutralisation; passive immunotherapy.
XX Synthetic.
XX
```

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PH Key Location/Qualifiers
FT Region 1..27
FT /label= FR1
FT Region 28..32
FT /label= CDR1
FT Region 33..46
FT /label= FR2
FT Region 47..63
FT /label= CDR2
FT Region 64..95
FT /label= FR3
FT Region 96..113
FT /label= CDR3
FT Region 114..124
FT /label= FR4
XX WO9511317-A1.
XX 27-APR-1995.
XX 19-OCT-1994; 94WO-US011907.
XX 19-OCT-1993; 93US-00139409.
XX 26-APR-1994; 94US-00233619.
XX 19-SEP-1994; 94US-00308841.
XX (SCRI ) SCRIPPS RES INST.
XX Barbas CF, Burton DR, Lerner RA;
XX WPI; 1995-170235/22.
XX Synthetic human neutralising monoclonal antibodies to human
XX immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
XX induced disease.
XX Example 4B1; Fig 7; 249pp; English.
XX The sequences given in AAR75604-09 represent human Fab's comprising
XX variable chain heavy regions (VH), which bind to HIV gp120. The six amino
XX acids which comprise CDR1 have been randomised with 3 of the six CDR1
XX sequences containing the preferred His residue as the first residue of
XX CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
XX used in the production of a human monoclonal antibody (Mab) which is
XX capable of immunoreacting with, and neutralising HIV. The Mab's are
XX capable of reducing HIV infectivity titre in an in vitro virus
XX infectivity assay by 50% at a concentration of <100 ng of antibody per
XX ml. They can be used to provide passive immunotherapy to HIV in a human.
XX They neutralise HIV more effectively than antibodies selected from non-
XX randomised combinatorial libraries
XX Sequence 124 AA;
XX Query Match 98.4%; Score 653; DB 2; Length 124;
XX Best Local Similarity 97.6%; Pred. No. 1e-59;
XX Matches 121; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGNKEFSAX 60
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFQFWMGWINPYNGNKEFSAX 60
QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYNDVWGKGTIV 120
DB 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYNDVWGKGTIV 120
QY 121 IVSS 124
DB 121 IVSS 124
RESULT 13
AAR54245
ID AAR54245 standard; protein; 124 AA.
```

```

XX AAR54245;
AC
XX
XX 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)
XX
XX Anti-HIV gp120 immunoglobulin heavy chain variable region b7.
XX
XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; heavy chain; variable region;
XX framework region; complementarity determining region.
XX
XX Homo sapiens.
OS
XX
XX
XX Location/Qualifiers
FH Key 1..27
FT Region /label= FR1
FT Region 28..32
FT Region /label= CDR1
FT Region 33..46
FT Region /label= FR2
FT Region 47..63
FT Region /label= CDR2
FT Region 64..95
FT Region /label= FR3
FT Region 96..113
FT Region /label= CDR3
FT Region 114..124
FT Region /label= FR4
XX
XX WO9407922-A1.
XX
XX 14-APR-1994.
XX
XX 30-SEP-1993; 93WO-US009328.
XX
XX 30-SEP-1992; 92US-00954148.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 1994-135516/16.
XX
XX New human monoclonal antibodies neutralising HIV - react with gp120 or
XX gp41 and nucleic acid encoding them, useful for in vivo or in vitro
XX diagnosis and for passive immuno-therapy.
XX
XX Claim 1; Page 164; 248pp; English.
XX
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
XX using primers specific for heavy and light chain variable regions. The
XX amplification products were inserted into a dicistronic vector to produce
XX a library of fragments. E.coli XL1 Blue cells were transformed with the
XX library. Filamentous phage were produced which expressed the MAb regions
XX on their surface. Panning with gp120 and gp41 resulted in the recovery of
XX immunoreactive clones. The heavy chain VH region sequence AAR54245
XX neutralises HIV1 gp120. (Updated on 25-MAR-2003 to Correct FN field.)
XX
XX Sequence 124 AA;
XX
XX Query Match 97.9%; Score 660; DB 2; Length 124;
XX Best Local Similarity 96.8%; Pred. No. 2.1e-59;
XX Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWROAPQGRFEWGWINPYNNGKFEFSAK 60
XX 1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWROAPQGRFEWGWINPYNNGKFEFSAK 60
XX
XX 61 FQDRVTFDTADTANTAYMEILRSADTAIYYCARVGPYTWDDSPQDNYMDVWGKGTIV 120
XX 61 FQDRVTFDTADTANTAYMEILRSADTAIYYCARVGPYTWDDSPQDNYMDVWGKGTIV 120
XX

```

```

OY 121 IVSS 124
DB 121 IVSS 124

RESULT 14
AAW01246
ID AAW01246 standard; protein; 124 AA.
XX
XX AAW01246;
AC
XX 28-JAN-1997 (first entry)
DT
XX
XX VH region of HIV neutralising MAb, IgG1 b7.
DE
XX
XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
XX anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Key 1..27
FT Region /label= FR1
FT Region 28..32
FT Region /label= CDR1
FT Region 33..46
FT Region /label= FR2
FT Region 47..63
FT Region /label= CDR2
FT Region 64..95
FT Region /label= FR3
FT Region 96..113
FT Region /label= CDR3
FT Region 114..124
FT Region /label= FR4
XX
XX WO9602273-A1.
XX
XX 01-FEB-1996.
XX
XX 11-JUL-1995; 95WO-US008743.
XX
XX 18-JUL-1994; 94US-00276852.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 1996-179601/18.
XX
XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
XX immunotherapy and detection of HIV infection.
XX
XX Example; Fig 10; 366pp; English.
XX
XX The sequences given in AAW01233-60 represent the heavy chain variable
XX regions (VH) of a series of monoclonal antibodies (MAb's) which are
XX immunoreactive with HIV glycoprotein gp120 and are capable of
XX neutralising HIV. This sequence represents the sequence of the JH6 gene
XX clone, b7. A MAb containing this VH sequence has the capacity to reduce
XX HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a
XX concentration of less than 700 ng of antibody/ml, and binds mature gp120
XX preferentially over the precursor gp160. The MAb may be used for
XX determining immunocompetence of a human anti-HIV antibody and in the
XX detection of HIV infection
XX
XX Sequence 124 AA;
XX
XX Query Match 97.9%; Score 660; DB 2; Length 124;
XX Best Local Similarity 96.8%; Pred. No. 2.1e-59;
XX Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX

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Thu Aug 26 14:28:11 2004

CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the antibodies
CC associated with monoclonal antibodies of xenogeneic or chimeric
CC derivation
XX
SQ Sequence 124 AA;
Query Match 97.9%; Score 660; DB 3; Length 124;
Best Local Similarity 96.8%; Pred. No. 2.1e-59;
Matches 120; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEFSK 60
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEFSK 60
QY 61 FQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGT 120
DB 61 FQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGT 120
QY 121 IVSS 124
DB 121 IVSS 124
RESULT 16
AA95098
ID AAY95098 standard; protein; 124 AA.
XX
AC AAY95098;
XX
DT 30-JUN-2000 (first entry)
XX
DE Anti-gp120 antibody heavy chain variable region from clone b7.
XX
KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN AU9948756-A.
XX
PD 17-FEB-2000.
XX
PF 16-SEP-1999; 99AU-00048756.
XX
PR 16-SEP-1999; 99AU-00048756.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
PS WPI; 2000-293393/26.
XX
PT Novel human monoclonal antibodies which immunoreact with and neutralize
PT human immunodeficiency virus useful for treating HIV infections.
XX
PS Example 9; Fig 10; 366pp; English.
XX
CC The present sequence represents a fragment of an anti-human
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
CC in vitro virus infectivity assay by 50%, at a concentration of less than
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
CC immunotherapy of HIV induced disease. They are useful as neutralising
CC field isolates and provide useful information regarding the

QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEFSK 60
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNKKEFSK 60
QY 61 FQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGT 120
DB 61 FQDRVTFTADTSANTAYMELRSLSADTAIVYCARVGPYSWDDSPQDNYMDVWGKGT 120
QY 121 IVSS 124
DB 121 IVSS 124
RESULT 15
AA98207
ID AAY98207 standard; protein; 124 AA.
XX
AC AAY98207;
XX
DT 04-JUL-2000 (first entry)
XX
DE Anti-gp120 antibody heavy chain variable region from clone b7.
XX
KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
KW passive immunotherapy; reduce severity; HIV-induced disease;
KW immunocompetence; active immunisation.
XX
OS Homo sapiens.
XX
PN AU9948754-A.
XX
PD 17-FEB-2000.
XX
PF 16-SEP-1999; 99AU-00048754.
XX
PR 16-SEP-1999; 99AU-00048754.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
PS WPI; 2000-246867/22.
XX
PT Human neutralizing monoclonal antibodies to human immunodeficiency virus
PT (HIV) used for providing passive immunotherapy to HIV are specific for
PT glycoprotein-120.
XX
PS Example 9; Fig 10; 374pp; English.
XX
CC This sequence represents a fragment of the antibodies of the invention.
CC The invention relates to the production of an anti-HIV (human
CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
CC of reducing an HIV infectivity titre in an in vitro virus infectivity
CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
CC production of the antibody comprises: (a) providing a first
CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
CC (which does not comprise the sequence represented by AAY98206) and a
CC second polynucleotide encoding a light chain immunoglobulin amino acid
CC sequence; (b) inserting the first and second polynucleotide sequences
CC into a host cell; (c) maintaining the host cell in conditions which allow
CC the amino acid sequences encoded by the polynucleotides to be expressed
CC in the host cell; and (d) isolating the antibody comprising the heavy and
CC light chain immunoglobulin amino acid sequences from the host cell. The
CC anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used for
CC neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting HIV
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active


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ID  AAW01247 standard; protein; 124 AA.
XX
AC  AAW01247;
XX
DT  28-JAN-1997 (first entry)
XX
DE  VH region of HIV neutralising MAb, IgG1 b21.
XX
KW  Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
KW  HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW  virus infectivity assay; precursor gp160; immunocompetence; human;
KW  anti-HIV antibody; detection; HIV infection.
XX
OS  Homo sapiens.
XX
FH  Key      Location/Qualifiers
FT  Region   1..27
FT  /label= FR1
FT  Region   28..32
FT  /label= CDR1
FT  Region   33..46
FT  /label= FR2
FT  Region   47..63
FT  /label= CDR2
FT  Region   64..95
FT  /label= FR3
FT  Region   96..113
FT  /label= CDR3
FT  Region   114..124
FT  /label= FR4
XX
PN  WO9602273-A1.
XX
PD  01-FEB-1996.
XX
PF  11-JUL-1995; 95WO-US008743.
XX
PR  18-JUL-1994; 94US-00276852.
XX
PA  (SRI ) SCRIPPS RES INST.
XX
PI  Burton DR, Barbas CF, Lerner RA;
XX
XX  WPI; 1996-179601/18.
XX
DR  Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
PT  immuno:therapy and detection of HIV infection.
XX
PS  Example; Fig 10; 366pp; English.
XX
CC  The sequences given in AAW01233-60 represent the heavy chain variable
CC  regions (VH) of a series of monoclonal antibodies (MAb's) which are
CC  immunoreactive with HIV glycoprotein gp120 and are capable of
CC  neutralising HIV. This sequence represents the sequence of the JH6 gene
CC  clone, b21. A MAb containing this VH sequence has the capacity to reduce
CC  HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a
CC  concentration of less than 700 ng of antibody/ml, and binds mature gp120
CC  preferentially over the precursor gp160. The MAb may be used for
CC  determining immunocompetence of a human anti-HIV antibody and in the
CC  detection of HIV infection
XX
XX  Sequence 124 AA;
XX
SQ
Query Match      97.3%; Score 656; DB 2; Length 124;
Best Local Similarity 96.0%; Pred. No. 5.4e-59;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY  1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSAK 60
DQ  1 LEQSGAEVKKPGASVKVSQASGYRFSNFIHWVROAPGQRFEMWGWINPYNGNKEFSAK 60
QY  61 FQDRVTFDTADTSANTAYMELSLRSTDTAIYCARVGPTWDDSPQDNYYMDVWGKGTKV 120
|||||

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Db  61 FQDRVTFDTADTSANTAYMELSLRSTDTAIYCARVGPTWDDSPQDNYYMDVWGKGTKV 120
QY  121 IVSS 124
    ||||
Db  121 IVSS 124

RESULT 21
AA98208
ID  AA98208 standard; protein; 124 AA.
XX
AC  AA98208;
XX
DT  04-JUL-2000 (first entry)
XX
DE  Anti-gp120 antibody heavy chain variable region from clone b21.
XX
KW  Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KW  human immunodeficiency virus type 1; HIV-1; infectivity titre;
KW  passive immunotherapy; reduce severity; HIV-induced disease;
KW  immunocompetence; active immunisation.
XX
OS  Homo sapiens.
XX
PN  AU9948754-A.
XX
PD  17-FEB-2000.
XX
PF  16-SEP-1999; 99AU-00048754.
XX
PR  16-SEP-1999; 99AU-00048754.
XX
PA  (SRI ) SCRIPPS RES INST.
XX
PI  Burton DR, Barbas CF, Lerner RA;
XX
XX  WPI; 2000-246867/22.
XX
DR  Human neutralizing monoclonal antibodies to human immunodeficiency virus
PT  (HIV) used for providing passive immunotherapy to HIV are specific for
PT  glycoprotein-120.
XX
PS  Example 9; Fig 10; 374pp; English.
XX
CC  This sequence represents a fragment of the antibodies of the invention.
CC  The invention relates to the production of an anti-HIV (human
CC  immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
CC  of reducing an HIV infectivity titre in an in vitro virus infectivity
CC  assay by 50% at a concentration of less than 70 ng/ml. The method for the
CC  production of the antibody comprises: (a) providing a first
CC  polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
CC  (which does not comprise the sequence represented by AA98206) and a
CC  second polynucleotide encoding a light chain immunoglobulin amino acid
CC  sequence; (b) inserting the first and second polynucleotide sequences
CC  into a host cell; (c) maintaining the host cell in conditions which allow
CC  the amino acid sequences encoded by the polynucleotides to be expressed
CC  in the host cell; and (d) isolating the antibody comprising the heavy and
CC  light chain immunoglobulin amino acid sequences from the host cell. The
CC  anti-HIV gp-120 monoclonal antibody is used for providing passive
CC  immunotherapy to HIV in a human. They can be administered to high-risk
CC  patients to reduce the likelihood and/or severity of HIV-induced disease
CC  and to patients who are already HIV-infected. The antibodies are used for
CC  neutralising field isolates which provides information about the
CC  immunocompetence of an immune response in HIV patients, for detecting HIV
CC  in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC  producing anti-idiotypic antibodies which can be used for active
CC  immunisation and to screen human monoclonal antibodies to identify those
CC  with the same binding specificity and to monitor the course of HIV
CC  disease therapy by measuring the changes in concentration of HIV present
CC  in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC  monoclonal antibodies are encoded by a human polynucleotide sequence and
CC  when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC  reduce the problems of significant host immune response to the antibodies

```

CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation
 XX
 SQ Sequence 124 AA;

Query Match 97.3%; Score 656; DB 3; Length 124;
 Best Local Similarity 96.0%; Pred. No. 5.4e-59;
 Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPQGFVWVGWNPYNGNKEFSK 60
 Db 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPQGFVWVGWNPYNGNKEFSK 60

QY 61 FQDRVTPTADTANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGT 120
 Db 61 FQDRVTPTADTANTAYMELRSLSRSTDTAIYICARVGPYTWDDSPQDNYMDVWGKGT 120

QY 121 IVSS 124
 Db 121 IVSS 124

RESULT 22

AA95099
 ID AAY95099 standard; protein; 124 AA.

AC AAY95099;

XX 30-JUN-2000 (first entry)

XX Anti-gp120 antibody heavy chain variable region from clone b21.

XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.

XX Homo sapiens.

XX AU9948756-A.

XX 17-FEB-2000.

XX 16-SEP-1999; 99AU-00048756.

XX 16-SEP-1999; 99AU-00048756.

XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;

XX WPI; 2000-293393/26.

XX Novel human monoclonal antibodies which immunoreact with and neutralize
 PT human immunodeficiency virus useful for treating HIV infections.

XX Example 9; Fig 10; 366pp; English.

XX The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantages of the

CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV

XX Sequence 124 AA;

Query Match 97.3%; Score 656; DB 3; Length 124;
 Best Local Similarity 96.0%; Pred. No. 5.4e-59;
 Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPQGFVWVGWNPYNGNKEFSK 60
 Db 1 LEQSGAEVKPGASVKVSCQASGYRFSNFIHWVRQAPQGFVWVGWNPYNGNKEFSK 60

QY 61 FQDRVTPTADTANTAYMELRSLSADTAVYICARVGPYSWDDSPQDNYMDVWGKGT 120
 Db 61 FQDRVTPTADTANTAYMELRSLSRSTDTAIYICARVGPYTWDDSPQDNYMDVWGKGT 120

QY 121 IVSS 124
 Db 121 IVSS 124

RESULT 23

AA975606
 ID AAR75606 standard; protein; 124 AA.

XX AAR75606;

XX 11-MAR-1996 (first entry)

XX VH Fab H4H1-5 binds to gp120.

XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
 KW 3b1; 3b3; 3b4; MT4; humanised; monoclonal antibody; MAb;
 KW immunoreaction; neutralisation; passive immunotherapy.

XX Synthetic.

Key	Location/Qualifiers
FT Region	1..27
FT	/label= FR1
FT Region	28..32
FT	/label= CDR1
FT Region	33..46
FT	/label= FR2
FT Region	47..63
FT	/label= CDR2
FT Region	64..95
FT	/label= FR3
FT Region	96..113
FT	/label= CDR3
FT Region	114..124
FT	/label= FR4

XX WO9511317-A1.

XX 27-APR-1995.

XX 19-OCT-1994; 94WO-US011907.

XX 19-OCT-1993; 93US-00139409.

XX 26-APR-1994; 94US-00233619.

XX 19-SEP-1994; 94US-00308841.

XX (SCRI) SCRIPPS RES INST.


```

XX PI Barbas CF, Burton DR, Lerner RA;
XX PN WPI; 1995-170235/22.
XX PD Synthetic human neutralising monoclonal antibodies to human
XX PT immunodeficiency virus - used for diagnosis and immunotherapy of HIV-
XX PT induced disease.
XX PS Example 4B1; Fig 7; 249pp; English.
XX PS The sequences given in AAR75604-09 represent human Fab's comprising
XX CC variable chain heavy regions (VH), which bind to HIV gp120. The six amino
XX CC acids which comprise CDR1 have been randomised with 3 of the six CDR1
XX CC sequences containing the preferred His residue as the first residue of
XX CC CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
XX CC used in the production of a human monoclonal antibody (MAB) which is
XX CC capable of immunoreacting with, and neutralising HIV. The MAB's are
XX CC capable of reducing HIV infectivity titre in an in vitro virus
XX CC infectivity assay by 50% at a concentration of <100 ng of antibody per
XX CC ml. They can be used to provide passive immunotherapy to HIV in a human.
XX CC They neutralise HIV more effectively than antibodies selected from non-
XX CC randomised combinatorial libraries
XX SQ Sequence 124 AA;
XX Query Match 97.2%; Score 655; DB 2; Length 124;
XX Best Local Similarity 97.6%; Pred. No. 6.8e-59;
XX Matches 121; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSAK 60
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSAK 60
QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 121 IVSS 124
DB 121 IVSS 124
RESULT 24
AAR75609
ID AAR75609 standard; protein; 124 AA.
XX AAR75609;
XX AC Human; Fab; variable chain; heavy; light; region; VH; HIV; gp120;
XX DT 11-MAR-1996 (first entry)
XX DE 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; MAB;
XX DE immunoreaction; neutralisation; passive immunotherapy.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Region 1..27
FT FT /label= FR1
FT FT 28..32
FT FT /label= CDR1
FT FT 33..46
FT FT /label= FR2
FT FT 47..63
FT FT /label= CDR2
FT FT 64..95
FT FT /label= FR3
FT FT 96..113
FT FT /label= CDR3
FT FT 114..124

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FT XX /label= FR4
XX PN WO95111317-A1.
XX PD 27-APR-1995.
XX XX 19-OCT-1994; 94WO-US011907.
XX PR 19-OCT-1993; 93US-00139409.
XX PR 26-APR-1994; 94US-00233619.
XX PR 19-SEP-1994; 94US-00308841.
XX XX (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Burton DR, Lerner RA;
XX XX WPI; 1995-170235/22.
XX PT Synthetic human neutralising monoclonal antibodies to human
XX PT immunodeficiency virus - used for diagnosis and immunotherapy of HIV-
XX PT induced disease.
XX PS Example 4B1; Fig 7; 249pp; English.
XX PS The sequences given in AAR75604-09 represent human Fab's comprising
XX CC variable chain heavy regions (VH), which bind to HIV gp120. The six amino
XX CC acids which comprise CDR1 have been randomised with 3 of the six CDR1
XX CC sequences containing the preferred His residue as the first residue of
XX CC CDR1 to avoid glycosylation, as occurs if Asn is present. These Fab's are
XX CC used in the production of a human monoclonal antibody (MAB) which is
XX CC capable of immunoreacting with, and neutralising HIV. The MAB's are
XX CC capable of reducing HIV infectivity titre in an in vitro virus
XX CC infectivity assay by 50% at a concentration of <100 ng of antibody per
XX CC ml. They can be used to provide passive immunotherapy to HIV in a human.
XX CC They neutralise HIV more effectively than antibodies selected from non-
XX CC randomised combinatorial libraries
XX SQ Sequence 124 AA;
XX Query Match 97.2%; Score 655; DB 2; Length 124;
XX Best Local Similarity 97.6%; Pred. No. 6.8e-59;
XX Matches 121; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSAK 60
DB 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFEMWGWINPYNGNKEFSAK 60
QY 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 61 FQDRVTFDTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
QY 121 IVSS 124
DB 121 IVSS 124
RESULT 25
AAR75572
ID AAR75572 standard; protein; 124 AA.
XX AAR75572;
XX AC Human; Fab; variable chain; heavy; light; region; VH; HIV; gp120;
XX DT 05-MAR-1996 (first entry)
XX DE VH Fab 3b9 binds to gp120.
XX DE Human; Fab; variable chain; heavy; light; region; VH; HIV; gp120;
XX KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; MAB;
XX KW immunoreaction; neutralisation; passive immunotherapy.
XX OS Synthetic.
XX FH Key Location/Qualifiers

```

```
FT Region 1. .27
FT /label= FR1
FT Region 28. .32
FT /label= CDR1
FT Region 33. .46
FT /label= FR2
FT Region 47. .63
FT /label= CDR2
FT Region 64. .95
FT /label= FR3
FT Region 96. .113
FT /label= CDR3
FT Region 114. .124
FT /label= FR4
XX WO9511317-A1.
XX
XX 27-APR-1995.
XX
XX 19-OCT-1994; 94WO-US011907.
XX
XX 19-OCT-1993; 93US-00139409.
XX 26-APR-1994; 94US-00233619.
XX 19-SEP-1994; 94US-00308841.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Barbas CF, Burton DR, Lerner RA;
XX
XX WPI; 1995-170235/22.
XX
XX Synthetic human neutralising monoclonal antibodies to human
XX immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
XX induced disease.
XX
XX Claim 6; Page 172-173; 249pp; English.
XX
XX The sequences given in AAR75568-72 represent human Fab's comprising
XX variable chain heavy regions (VH), which bind to HIV gp120. The Fab's
XX 3b1, 3b3, 3b4 and 3b9 have the same amino acid composition as MT4 but
XX have randomised amino acids in the entire CDR1 and in four of the 18
XX amino acid residues in CDR3. These Fab's are used in the production of a
XX human monoclonal antibody (MAB) which is capable of immunoreacting with,
XX and neutralising HIV. The MAB's are capable of reducing HIV infectivity
XX titre in an in vitro virus infectivity assay by 50% at a concentration of
XX <100 ng of antibody per ml. They can be used to provide passive
XX immunotherapy to HIV in a human. They neutralise HIV more effectively
XX than antibodies selected from non-randomised combinatorial libraries
XX
XX Sequence 124 AA;
XX
XX Query Match 96.9%; Score 653; DB 2; Length 124;
XX Best Local Similarity 96.0%; Pred. No. 1.le-58;
XX Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 LEQSGAEVKPGASVKVSCQASGYRFSNFTVHWVRQAPGQRFQFWMGWINPYNGKFSK 60
XX |||||
XX 1 LEQSGAEVKPGASVKVSCQASGYRFSNFTVHWVRQAPGQRFQFWMGWINPYNGKFSK 60
XX |||||
XX 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
XX |||||
XX 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPWDDSPQDNYMDVWGKGTIV 120
XX |||||
XX 121 IVSS 124
XX |||||
XX 121 IVSS 124
XX
XX RESULT 26
XX AAR75570
XX ID AAR75570 standard; protein; 124 AA.
XX
XX AAR75570;
```

```
XX 05-MAR-1996 (first entry)
XX
XX VH Fab 3b3 binds to gp120.
XX
XX Human; Fab; variable chain; heavy; light; region; VH; HIV; gp120;
XX 3b1, 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; MAb;
XX immunoreaction; neutralisation; passive immunotherapy.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Region 1. .27
XX /label= FR1
XX Region 28. .32
XX /label= CDR1
XX Region 33. .46
XX /label= FR2
XX Region 47. .63
XX /label= CDR2
XX Region 64. .95
XX /label= FR3
XX Region 96. .113
XX /label= CDR3
XX Region 114. .124
XX /label= FR4
XX
XX WO9511317-A1.
XX
XX 27-APR-1995.
XX
XX 19-OCT-1994; 94WO-US011907.
XX
XX 19-OCT-1993; 93US-00139409.
XX 26-APR-1994; 94US-00233619.
XX 19-SEP-1994; 94US-00308841.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Barbas CF, Burton DR, Lerner RA;
XX
XX WPI; 1995-170235/22.
XX
XX Synthetic human neutralising monoclonal antibodies to human
XX immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
XX induced disease.
XX
XX Claim 6; Page 171; 249pp; English.
XX
XX The sequences given in AAR75568-72 represent human Fab's comprising
XX variable chain heavy regions (VH), which bind to HIV gp120. The Fab's
XX 3b1, 3b3, 3b4 and 3b9 have the same amino acid composition as MT4 but
XX have randomised amino acids in the entire CDR1 and in four of the 18
XX amino acid residues in CDR3. These Fab's are used in the production of a
XX human monoclonal antibody (MAB) which is capable of immunoreacting with,
XX and neutralising HIV. The MAB's are capable of reducing HIV infectivity
XX titre in an in vitro virus infectivity assay by 50% at a concentration of
XX <100 ng of antibody per ml. They can be used to provide passive
XX immunotherapy to HIV in a human. They neutralise HIV more effectively
XX than antibodies selected from non-randomised combinatorial libraries
XX
XX Sequence 124 AA;
XX
XX Query Match 96.7%; Score 652; DB 2; Length 124;
XX Best Local Similarity 96.0%; Pred. No. 1.4e-58;
XX Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 LEQSGAEVKPGASVKVSCQASGYRFSNFTVHWVRQAPGQRFQFWMGWINPYNGKFSK 60
XX |||||
XX 1 LEQSGAEVKPGASVKVSCQASGYRFSNFTVHWVRQAPGQRFQFWMGWINPYNGKFSK 60
XX |||||
XX 61 FQDRVTFTADTSANTAYMELSLRSADTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
XX |||||
```

```

Db 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGEWGWDSDSPQDNYNDVWGKGTIV 120
QY 121 IVSS 124
Db 121 IVSS 124
Db 121 IVSS 124

RESULT 27
AAY44346
ID AAY44346 standard; protein; 250 AA.
AC AAY44346;
DT 14-MAR-2000 (first entry)
DE 3B3 antibody.
KW 3B3 antibody; immunotoxin; variable fragment; Fv; gp120 coat protein;
KW exotoxin; PE38; Human immunodeficiency virus type 1; HIV-1; specificity;
KW combinatorial phage display library; bone marrow RNA; connector peptide;
KW cytotoxic moiety; transformed cell line; transplant; quantify.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 129..143
FT /label= Linker peptide
FT /note= "Links VH and VL regions of 3B3 antibody"
XX WO9964073-A2.
XX 16-DEC-1999.
XX 08-JUN-1999; 99WO-US012909.
XX 11-JUN-1998; 98US-0088860P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Pastan IH, Bera TK, Kennedy PE, Berger EA, Barbas CF;
XX WPI; 2000-105833/09.
XX N-PSDB; AAZ29448.
XX Novel recombinant immunotoxin directed against the HIV- 1 gp120 coat
XX protein useful for treating HIV-1 infections.
XX Claim 17; Page 47; 50pp; English.
XX The present amino acid sequence is the variable fragment (Fv) of 3B3
XX antibody, isolated from a combinatorial phage display library constructed
XX from bone marrow RNA of an infected individual. It is used in a novel
XX chimeric immunotoxin, that comprises an anti-gp120 antibody, having
XX binding specificity to 3B3(Fv) antibody, that is attached by a connector
XX peptide to a cytotoxic moiety, PE38 derived from P.aeruginosa. The
XX chimeric immunotoxin is used in the treatment of HIV-1 infections. It is
XX capable of specifically targeting and killing cells displaying HIV-1
XX gp120 coat protein. They can be used ex vivo to reduce and/or eliminate
XX the HIV viral load in the infected cells. It can also be used in
XX establishing transformed cell lines derived from HIV-infected sources.
XX The immunotoxins can also be used for detecting the presence or absence
XX and for quantifying the infected cells
XX Sequence 250 AA;
Query Match 96.7%; Score 652; DB 3; Length 250;
Best Local Similarity 96.0%; Pred. No. 3.le-58;
Matches 119; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 LEQSGAEVKPGASVKVSCQASGYSFNSFVTHVRQAPGQRFEMWGWINPYNGKFSK 60
Db 5 LEQSGAEVKPGASVKVSCQASGYSFNSFVTHVRQAPGQRFEMWGWINPYNGKFSK 64

```

```

QY 61 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGPYSWDDSPQDNYNDVWGKGTIV 120
Db 65 FQDRVTFTADTSANTAYMELSLRSADTAVYYCARVGEWGWDSDSPQDNYNDVWGKGTIV 124
QY 121 IVSS 124
Db 125 IVSS 128

RESULT 28
AAR54335
ID AAR54335 standard; protein; 124 AA.
XX AAR54335;
XX 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin L12-HC12 shuffled heavy chain.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; heavy chain; shuffled;
KW variable region; framework; complementarity determining region.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Region 1..31
FT /label= FR1
FT Region 32..36
FT /label= CDR1
FT Region 37..50
FT /label= FR2
FT Region 51..67
FT /label= CDR2
FT Region 68..99
FT /label= FR3
FT Region 100..117
FT /label= CDR3
FT Region 118..124
FT /label= FR4
XX WO9407922-A1.
XX 14-APR-1994.
XX 30-SEP-1993; 93WO-US009328.
XX 30-SEP-1992; 92US-00954148.
XX (SCRI ) SCRIPPS RES INST.
XX Burton DR, Barbas CF, Lerner RA;
XX WPI; 1994-135516/16.
XX New human monoclonal antibodies neutralising HIV - react with gp120 or
XX gp41 and nucleic acid encoding them, useful for in vivo or in vitro
XX diagnosis and for passive immuno-therapy.
XX Example; Page 206-207; 248pp; English.
XX The anti-HIV gp120 light chain clone b12 (AAR54253) was recombined with a
XX heavy chain library to construct a new library L12-HCn. Ten heavy chains
XX which recombined with the b12 light chain and bound gp120 by panning were
XX chosen for sequence analysis. AAR54335 was one of these heavy chains.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 124 AA;
Query Match 95.8%; Score 646; DB 2; Length 124;
Best Local Similarity 96.7%; Pred. No. 5.6e-58;
Matches 116; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```


CC and to patients who are already HIV-infected. The antibodies are used for
CC neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting HIV
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the antibodies
CC associated with monoclonal antibodies of xenogeneic or chimeric
XX derivation
SQ Sequence 124 AA;

Query Match 95.8%; Score 646; DB 3; Length 124;
Best Local Similarity 96.7%; Pred. No. 5.6e-58;
Matches 116; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWRQAPQRFQWGMWNPYNGNKEFSAK 60
DB 5 LEQSGAEVKKPGASVKVSCQASGYRFSNFIHWRQAPQRFQWGMWNPYNGNKEFSAK 64
QY 61 FQDRVTFDTADTSANTAYMELRSLSRSDTAVYCARVGPYSWDDSPQDNYMDVWGKGTIV 120
DB 65 FQDRVTFDTADTSANTAYMELRSLSRSDTAVYCARVGPYTWDDSPQDNYMDVWGKGTIV 124

Search completed: August 26, 2004, 13:37:42
Job time : 49.4667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2004, 13:33:57 ; Search time 38.3926 Seconds
(without alignments)
1199.858 Million cell updates/sec

Title: US-10-016-986-155
Perfect score: 793
Sequence: 1 MEWSWVLEFLSVTCVHSQ.....PODNYMDVWGKGTIVSS 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTRMBL-25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	497	62.7	614	Q96GA6	Q96GA6 homo sapien
2	483.5	61.0	500	Q9BRV0	Q9BRV0 homo sapien
3	471.5	59.5	159	Q96QSO	Q96QSO homo sapien
4	468.5	59.1	613	Q8VCX7	Q8VCX7 mus musculus
5	468	59.0	168	Q8VDC9	Q8VDC9 mus musculus
6	453.5	57.2	473	Q91L25	Q91L25 mus musculus
7	448.5	56.6	469	Q7Z7P5	Q7Z7P5 homo sapien
8	445	56.1	437	Q8WY24	Q8WY24 homo sapien
9	441	55.6	489	Q8VCX4	Q8VCX4 mus musculus
10	440	55.5	470	Q7TMK1	Q7TMK1 mus musculus
11	440	55.5	473	Q9D8L4	Q9D8L4 mus musculus
12	428	54.0	481	Q91WT1	Q91WT1 mus musculus
13	425	53.6	150	Q9Y298	Q9Y298 homo sapien
14	423	53.3	468	Q91L31	Q91L31 mus musculus
15	416.5	52.5	481	Q8VCV5	Q8VCV5 mus musculus
16	412.5	52.0	463	Q99LC4	Q99LC4 mus musculus

17	412	52.0	119	5	Q9GYZ2	Q9GYZ2 schistosoma
18	412	52.0	480	11	Q8K0Z4	Q8K0Z4 mus musculus
19	411.5	51.9	278	11	Q921K1	Q921K1 mus musculus
20	407.5	51.4	482	11	Q8K172	Q8K172 mus musculus
21	407.5	51.4	488	11	Q8K0F2	Q8K0F2 mus musculus
22	407	51.3	119	4	Q9UL94	Q9UL94 homo sapien
23	406.5	51.3	124	4	Q9UL92	Q9UL92 homo sapien
24	405.5	51.1	488	11	Q91WR1	Q91WR1 mus musculus
25	405.5	51.1	125	4	Q9UL95	Q9UL95 homo sapien
26	400	50.4	614	11	Q7TWT6	Q7TWT6 mus musculus
27	398.5	50.3	496	4	Q6DK0	Q6DK0 homo sapien
28	398	50.2	157	4	Q95978	Q95978 homo sapien
29	398	50.2	474	11	Q8R3H6	Q8R3H6 mus musculus
30	395	49.8	484	11	Q91LA6	Q91LA6 mus musculus
31	382.5	48.2	116	4	Q9UL89	Q9UL89 homo sapien
32	371	46.8	481	11	Q91WT3	Q91WT3 mus musculus
33	364.5	46.0	145	11	Q924R3	Q924R3 mus musculus
34	364	45.9	142	11	Q924Q1	Q924Q1 mus musculus
35	362.5	45.7	143	11	Q924R0	Q924R0 mus musculus
36	362	45.6	144	11	Q924P5	Q924P5 mus musculus
37	358.5	45.2	143	11	Q924Q5	Q924Q5 mus musculus
38	357.5	45.1	145	11	Q924R4	Q924R4 mus musculus
39	355	44.8	146	11	Q924Q3	Q924Q3 mus musculus
40	355	44.8	147	11	Q925R3	Q925R3 mus musculus
41	354.5	44.7	109	11	Q9UL75	Q9UL75 mus musculus
42	354.5	44.7	143	11	Q91V67	Q91V67 mus musculus
43	354	44.6	117	11	Q9QX70	Q9QX70 mus musculus
44	353.5	44.6	145	11	Q924Q6	Q924Q6 mus musculus
45	353	44.5	117	11	Q9QX69	Q9QX69 mus musculus
46	352.5	44.5	145	11	Q924Q7	Q924Q7 mus musculus
47	352.5	44.5	145	11	Q924R1	Q924R1 mus musculus
48	352	44.4	146	11	Q924R8	Q924R8 mus musculus
49	348.5	43.9	145	11	Q924Q9	Q924Q9 mus musculus
50	348	43.9	140	11	Q924P8	Q924P8 mus musculus
51	347.5	43.8	143	11	Q924R7	Q924R7 mus musculus
52	346.5	43.7	241	11	Q921A6	Q921A6 mus musculus
53	346	43.6	140	11	Q924R2	Q924R2 mus musculus
54	345.5	43.6	141	11	Q924Q4	Q924Q4 mus musculus
55	345.5	43.6	145	11	Q924F7	Q924F7 mus musculus
56	342.5	43.2	143	11	Q91VA2	Q91VA2 mus musculus
57	341.5	43.1	137	11	Q924R6	Q924R6 mus musculus
58	341.5	43.1	143	11	Q924Q0	Q924Q0 mus musculus
59	339.5	42.8	118	11	Q921C4	Q921C4 mus musculus
60	339	42.7	123	11	Q8V1J1	Q8V1J1 mus musculus
61	337.5	42.6	613	4	Q8WUX1	Q8WUX1 homo sapien
62	335.5	42.3	143	11	Q924P9	Q924P9 mus musculus
63	335.5	42.3	573	4	Q8WU38	Q8WU38 homo sapien
64	335	42.2	146	11	Q924Q8	Q924Q8 mus musculus
65	335	42.2	170	11	Q925R2	Q925R2 mus musculus
66	331	41.7	142	11	Q924Q2	Q924Q2 mus musculus
67	329.5	41.6	243	11	Q7TOM2	Q7TOM2 mus musculus
68	328	41.4	111	11	Q9D9B8	Q9D9B8 mus musculus
69	328	41.4	479	11	Q91WP5	Q91WP5 mus musculus
70	327	41.2	499	4	Q8N5K4	Q8N5K4 homo sapien
71	326.5	41.2	143	11	Q924P6	Q924P6 mus musculus
72	326	41.1	120	11	Q920E8	Q920E8 mus musculus
73	324.5	40.9	114	11	Q9JL81	Q9JL81 mus musculus
74	324.5	40.9	139	11	Q924R5	Q924R5 mus musculus
75	320.5	40.4	110	11	Q9JL77	Q9JL77 mus musculus
76	318.5	40.2	136	11	Q7TPE3	Q7TPE3 mus musculus
77	317	40.0	484	11	Q8VEA0	Q8VEA0 mus musculus
78	315	39.7	121	11	Q8CGS2	Q8CGS2 mus musculus
79	313.5	39.5	218	11	Q925S1	Q925S1 mus musculus
80	313	39.5	493	4	Q8NCL6	Q8NCL6 homo sapien
81	313	39.5	597	4	Q96BB9	Q96BB9 homo sapien
82	310	39.1	109	11	Q9JL85	Q9JL85 mus musculus
83	309	39.0	482	4	Q7Z351	Q7Z351 homo sapien
84	308	38.8	117	11	Q9ZIC6	Q9ZIC6 mus musculus
85	297.5	37.5	110	11	Q9JL83	Q9JL83 mus musculus
86	295.5	37.3	473	11	Q91Z05	Q91Z05 mus musculus
87	295	37.2	113	4	Q9UL90	Q9UL90 homo sapien
88	294.5	37.1	487	11	Q99KA4	Q99KA4 mus musculus
89	294	37.1	521	4	Q8N4Y9	Q8N4Y9 homo sapien

90 293 36.9 588 4 Q8WDX4
 Q96GA6 91 293 36.9 597 4 Q9BUL0
 AC Q96GA6; 92 293 36.9 618 4 Q96AA6
 DT 01-DEC-2001 (TrEMBLrel. 19, Created) 93 292 36.8 469 11 Q8R3V9
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 94 290.5 36.6 298 11 Q9QYF0
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 95 290 36.6 487 11 Q8QZ17
 DE Hypothetical protein. 96 289.5 36.5 147 4 Q9V509
 OS Homo sapiens (Human). 97 289 36.4 480 11 Q91XE1
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; 98 289 36.4 597 4 Q9BQB8
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 99 288 36.3 116 4 Q9UL93
 NCBI_TaxID=9606; 100 284.5 35.9 494 4 Q96K68

ALIGNMENTS

RESULT 1
 Q96GA6 ID Q96GA6 PRELIMINARY; PRT; 614 AA.
 AC Q96GA6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC009851; AAH09851.1; -
 DR PIR; S15590; S15590.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000005; HTHARAC.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
 DR PROSITE; PS00835; IG LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 614 AA; 67921 MW; 55EP536E77AA9BBB CRC64;
 Query Match 62.7%; Score 497; DB 4; Length 614;
 Best Local Similarity 63.0%; Pred. No. 5.8e-44;
 Matches 92; Conservative 17; Mismatches 31; Indels 6; Gaps 1;
 QY 1 MEWSWVFLFLLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
 Db 1 MDWTWRLFLVAATAAYDSQVQLVQSGAEVKKPGASVKVSCKASGTFYRILHWVRQAP 60
 QY 61 GQPFWMGWINPYNGNKEFSAKFDQRTVTFADTSANTAYMELSLRSADTAVYICARVGP 120
 Db 61 GQALEWGWITPENGNTNQAQKQDRVTITPDRSMNTAYMELSLRSADTAVYICARGYS 120
 QY 121 YSWDDSPQDNYNDVVGKGTITVSS 146
 Db 121 SSWDDA-----FDWGQGINVTIVSS 140

RESULT 2
 Q9BRV0 ID Q9BRV0 PRELIMINARY; PRT; 500 AA.
 AC Q9BRV0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005951; AAH05951.1; -
 DR HSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 500 AA; 54154 MW; 0A9BP43P2A3CC6D9 CRC64;
 Query Match 61.0%; Score 483.5; DB 4; Length 500;
 Best Local Similarity 63.9%; Pred. No. 1.2e-42;
 Matches 94; Conservative 12; Mismatches 40; Indels 1; Gaps 1;
 QY 1 MEWSWVFLFLLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
 Db 1 MDWTWRLFLVAATAAYDSQVQLVQSGAEVMSFGASVSVCKTSGYAFHYISIIWVRQAP 60
 QY 61 GQPFWMGWINPYNGNKEFSAKFDQRTVTFADTSANTAYMELSLRSADTAVYICARVGP 119
 Db 61 GQGLEWGWISPSDNTFRFAKFGQRTVLTDTSTVYMELSLRSDDTAVYICARRYC 120
 QY 120 PYSWDDSPQDNYNDVVGKGTITVSS 146
 Db 121 SYSSQNDYFYNDVVGKGTITVSS 147
 RESULT 3
 Q96QSO ID Q96QSO PRELIMINARY; PRT; 159 AA.
 AC Q96QSO;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative matrix cell adhesion molecule-3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tilson M.D.;
 RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
 mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY039025; AAK62649.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 SQ SEQUENCE 159 AA; 17497 MW; 5D29537B881FAF02 CRC64;
 Query Match 59.5%; Score 471.5; DB 4; Length 159;
 Best Local Similarity 61.7%; Pred. No. 5.5e-42;
 Matches 92; Conservative 18; Mismatches 36; Indels 3; Gaps 1;
 QY 1 MEWSWVFLFLLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
 Db 1 MDWTWRLFLVAATAAYDSQVQLVQSGAEVKKPGASVKVSCKASGYTFSSNYMWRQAP 60

QY 121 YSMDSDSPQDNYMDVWGKGTIVVSS 146
 Db 121 IYVG---YGLYFDYWGQGTITVSS 143

RESULT 7

Q7Z7P5 PRELIMINARY; PRT; 469 AA.
 AC Q7Z7P5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalak U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC051328; AAH51328.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 56.6%; Score 448.5; DB 4; Length 469;
 Best Local Similarity 56.3%; Pred. No. 5.8e-39;
 Matches 85; Conservative 21; Mismatches 28; Indels 17; Gaps 2;
 QY 1 MENSWFLPFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
 Db 1 MDWTWRLFLVAATGARPQVHLVQSGAEVKKPGASVKLSCKTSYRFSNFIHWVRQAP 60
 QY 61 GQRFEMWGNIPYNGNKEFSAKQDRVTFTADTSANTAYMELSLRSADTAVYVCARV- 116
 Db 61 GQGLEWGWISAHNGDTKYARKEQGRVTWTTDSATTSYMEFRSLRSDDTALFYCATKSR 120
 QY 117 -RVGPTSWDSDPDNYMDVWGKGTIVVSS 146
 Db 121 GQVGDF-----DSWGGQGLTVTVSS 139

RESULT 8

Q8WY24 PRELIMINARY; PRT; 497 AA.
 AC Q8WY24;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SNC66 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
 RT "Identification and characterization of SNC66, a Ig-like gene which is
 RT down-regulated in colorectal cancer";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF283666; AAL36987.1; -
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; IG_4.
 DR SMART: SM00406; IGV; 4.
 DR PROSITE: PS50835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 1.
 SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;
 Query Match 56.1%; Score 445; DB 4; Length 497;
 Best Local Similarity 56.2%; Pred. No. 1.5e-38;
 Matches 86; Conservative 16; Mismatches 35; Indels 16; Gaps 2;
 QY 1 MENSWFLPFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
 Db 1 MDWTWRLFLVAATGARPQVHLVQSGAEVKKPGASVKLSCKTSYRFSNFIHWVRQAP 60
 QY 61 GQRFEMWGNIPYNGNKEFSAKQDRVTFTADTSANTAYMELSLRSADTAVYVCARV- 119
 Db 61 GQGLEWGWGNIPQNTGTEFAKQGRITFSDTSTNTAYMVLSSLSDSAIYFCARGNL 120
 QY 120 -----PYSWDDSDPDNYMDVWGKGTIVVSS 146
 Db 121 RGRGRGFGYNW-----FDPWGHGTLTVVSS 144
 RESULT 9
 Q8VCX4 PRELIMINARY; PRT; 489 AA.
 AC Q8VCX4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN IGH-VJ558 OR A1893585.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC018322; AAH18322.1; -
 DR MGI: 96486; Igh-VJ558.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG; 4.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 489 AA; 53208 MW; CC85B1194DAFEF2C CRC64;

Query Match 55.6%; Score 441; DB 11; Length 489;
 Best Local Similarity 55.0%; Pred. No. 3.8e-38;
 Matches 83; Conservative 23; Mismatches 33; Indels 12; Gaps 2;

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QY 1 MEWSWVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYSRFSNFIHWVRQAP 60
Db 1 MEWCWVFLFLSVTTAGVHSGVQLVQSGAEVKKPGASVKLSCKASGYTFSDYFIHWIKQRS 60
QY 61 GORFPMWGNLPYNGNKEPKAQDRVTFADTSANTAYMELRSLSADTAVVYCARVGP 120
Db 61 GQGLEWIGNPNPSSGSIKFKNEKFKATLTADKSSITVYMDLSRLSLSADSVYFCAR--- 117
QY 121 YSWDDSPQDNY-----YMDVWGKGTIVVSS 146
Db 118 ---HEDRGNYGSLAWFWYWGQGLTVTSA 144

RESULT 10
Q7TMKL PRELIMINARY; PRT; 470 AA.
AC Q7TMKL;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE Hypothetical protein.
CS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RX MEDLINE=2238822; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Parner A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohnyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Stodgren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.C., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 2
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055910; AAH5910.1; -.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;

Query Match 55.5%; Score 440; DB 11; Length 470;
Best Local Similarity 57.5%; Pred. No. 4.6e-38;
Matches 84; Conservative 22; Mismatches 34; Indels 6; Gaps 2;

QY 1 MEWSWVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYSRFSNFIHWVRQAP 60
Db 1 MGWSWVFLFLSVTTAGVLSVQLQSGPELVKPGASVKLSCKASGYTFGYVHWVQKSH 60
QY 61 GORFPMWGNLPYNGNKEPKAQDRVTFADTSANTAYMELRSLSADTAVVYCARVGP 120
Db 61 GKSLWIGLVPNGDTSYNGKFKGKATLTADKSSITAYMELNSLSADSVYFCAR--- 117
QY 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
Db 118 YYISGS---YWFEDVWGAGTIVVSS 140

RESULT 12
Q91WT1 PRELIMINARY; PRT; 481 AA.
ID Q91WT1
AC Q91WT1;

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RESULT 11
Q9D8L4 PRELIMINARY; PRT; 473 AA.
ID Q9D8L4;
AC Q9D8L4;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE 1810060009rik protein.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Buit C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustingich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -.
DR PIR; S26746; S26746.
DR HSP; F01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 9BDE57A514475FBB CRC64;

Query Match 55.5%; Score 440; DB 11; Length 473;
Best Local Similarity 57.5%; Pred. No. 4.7e-38;
Matches 84; Conservative 24; Mismatches 30; Indels 8; Gaps 2;

QY 1 MEWSWVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYSRFSNFIHWVRQAP 60
Db 1 MEWSWVFLFLSVTTAGVHSGVQLVQSGAEVKKPGASVKISCKASGYTFDYIINWKQRP 60
QY 61 GORFPMWGNLPYNGNKEPKAQDRVTFADTSANTAYMELRSLSADTAVVYCARVGP 120
Db 61 GQGLEWIGKIPGSGSTYNEKFKGKATLTADKSSITAYMQLSLSADSVYFCARSG- 119
QY 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
Db 120 YDYD-----WFAVWGQGLTVTSA 138

RESULT 12
Q91WT1 PRELIMINARY; PRT; 481 AA.
ID Q91WT1
AC Q91WT1;

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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 54.08; Score 428; DB 11; Length 481;
Best Local Similarity 54.18; Pred. No. 8.9e-37;
Matches 79; Conservative 25; Mismatches 32; Indels 10; Gaps 1;

Qy 1 M EWSVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 M GMEWIFLLSGTAGVQCQQLQSGPELVKPGASVKISCKASGYRFTSYIHWVKRQP 60
Qy 61 GQRFEMWGNINPYNGNKEFSAKFDQRTVFTADTSANTAYMELSLRSADTAVYVCARVGP 120
Db 61 GQGLWGWIGVPGDGNKYNEKFKGKTLTADKSSSTAYMFLSLTSSESAVYFCTRGGG 120
Qy 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
Db 121 WAF-----DYWGQGTITLVSS 136
Qy 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
Db 121 YSG-----YDYWGQGTITLVSS 138

RESULT 13
QyY298 QY298 PRELIMINARY; PRT; 150 AA.
ID QY298
AC QY298;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IG V protein precursor (fragment).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98322155; PubMed=9657749;
RX Jacquemin M.G., Vander Elst L.P.L.;
RA "Mechanism and kinetics of factor VIII inactivation: study with an
RT IgG4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor.";
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CAA11829.1; -.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016489; F:immunoglobulin receptor activity; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Signal.

FT SIGNAL 1 19 POTENTIAL.
FT NON TER 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 53.64; Score 425; DB 4; Length 150;
Best Local Similarity 55.58; Pred. No. 4.4e-37;
Matches 81; Conservative 20; Mismatches 35; Indels 10; Gaps 1;

Qy 1 M EWSVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 M DMTWRIILFLVAAATGTHAQVLQSGAEVKKPGASVKVSCKVSGYTLTLPVHWVQAP 60
Qy 61 GQRFEMWGNINPYNGNKEFSAKFDQRTVFTADTSANTAYMELSLRSADTAVYVCARVGP 120
Db 61 KGLEWVGSGFDPESGESYIAREFQGSVTMTADTDTIAYMELSLRSDDTAVYICAVPDP 120
Qy 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
Db 121 DAF-----DIWGQGTIVVSS 136

RESULT 14
QyY298 QY298 PRELIMINARY; PRT; 468 AA.
ID QY298
AC QY298;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR PDB; 2AP2; 24-NOV-99.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 53.34; Score 423; DB 11; Length 468;
Best Local Similarity 53.44; Pred. No. 2.9e-36;
Matches 78; Conservative 26; Mismatches 34; Indels 8; Gaps 1;

Qy 1 M EWSVFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 M KCSWVIFFLMAVIGVNSEVQLQSGNELVPGASVKLSCTASGFNIKDSLMEHWKQP 60
Qy 61 GQRFEMWGNINPYNGNKEFSAKFDQRTVFTADTSANTAYMELSLRSADTAVYVCARVGP 120
Db 61 EQGLEWIGWIDPEGETKYAPQDKATITADTSSNTAYLQLSLTSEDTAIYTCARNLL 120
Qy 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
Db 121 YGG-----YDYWGQGTITLVSS 138

RESULT 15
QyY298 QY298 PRELIMINARY; PRT; 481 AA.
ID QY298
AC QY298;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
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RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029188; AAH29188.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG CI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGCI; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
SQ SEQUENCE 480 AA; 51645 MW; 8690A63C669CDBED CRC64;

Query Match 52.0%; Score 412; DB 11; Length 480;
Best Local Similarity 52.7%; Pred. No. 4.4e-35;
Matches 78; Conservative 26; Mismatches 30; Indels 14; Gaps 2;

Qy 1 MENSWVFLFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFGSFNFIHWVRQAP 60
Db 1 MGRWIFLFLSGTAGVHCQVQLQSGPELVKFGALVKISKASGYTFTSFDISNWKQRP 60

Qy 61 GQRFEMGWINPYNGKFEKSAKQDRVTFADTSANTAYMELSLRSADTAVYYCAR--V 118
Db 61 GQGPENIGWISPGDSSEYNEKFKGKATLTADKSSNTAYMHLSSLTSSENSAVYFCARSKL 120.

Qy 119 GPYSWDDSPQDNYMDVWGKGTIVVSS 146
Db 121 GGFAY-----WGQGLTVTUSA 136

RESULT 19
Q921K1 PRELIMINARY; PRT; 278 AA.
AC Q921K1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAH12207.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 278 AA; 29778 MW; F894P955DDCD948A CRC64;

Query Match 51.9%; Score 411.5; DB 11; Length 278;
Best Local Similarity 53.4%; Pred. No. 2.5e-35;
Matches 78; Conservative 24; Mismatches 37; Indels 7; Gaps 2;

Qy 1 MENSWVFLFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFGSFNFIHWVRQAP 60
Db 1 MGNWCIILFLVATATGVHSQVQLQPGAEIVKPGASVKLSCKASGYTFTSYWGHVQQR 60

Qy 61 GQRFEMGWINPYNGKFEKSAKQDRVTFADTSANTAYMELSLRSADTAVYYCARVGP 120
Db 61 GQGLEWICINPNISGGTNYNEKFKKATLAVDKSSSTVYMQLSLTSSEDSAVYYCTR--G 118

Qy 121 YSWDDSPQDNYMDVWGKGTIVVSS 146

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Db 119 YGYDD-----VYFDVWGAGTTVTVSS 139

RESULT 20
Q8K172 PRELIMINARY; PRT; 482 AA.
AC Q8K172;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to expressed sequence AI893595.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028249; AAH28249.1; -.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG CI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00407; IGCI; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
SQ SEQUENCE 482 AA; 52121 MW; A06FF083E771D084 CRC64;

Query Match 51.4%; Score 407.5; DB 11; Length 482;
Best Local Similarity 52.1%; Pred. No. 1.3e-34;
Matches 76; Conservative 25; Mismatches 36; Indels 9; Gaps 1;

Qy 1 MENSWVFLFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFGSFNFIHWVRQAP 60
Db 1 MGNWCIILFLVATATGVHSQVQLQPGAEIVKPGASVKLSCKASGYTFTSYWGHVQQR 60

Qy 61 GQRFEMGWINPYNGKFEKSAKQDRVTFADTSANTAYMELSLRSADTAVYYCARVGP 120
Db 61 GRGLEWIGRIDPNISGGTNYNEKFKKATLTVDKPSSTAYMQLSLTSSEDSAVYYCTREGD 120

Qy 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
Db 121 YD-----AMDYWGQGTSTVTVSS 137

RESULT 21
Q8K0F2 PRELIMINARY; PRT; 488 AA.
AC Q8K0F2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 Similar to expressed sequence A1893585.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 RQ TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR ENBL: BC031703, AAH31703.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SMO0407; IGc1; 3.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 2.
 SQ SEQUENCE 488 AA; 53127 MW; 0E3B156E155733F0 CRC64;
 Query Match 51.4%; Score 407.5; DB 11; Length 488;
 Best Local Similarity 52.7%; Pred. No. 1.4e-34;
 Matches 77; Conservative 26; Mismatches 40; Indels 3; Gaps 1;
 QY 1 MEWSVFLPFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
 DB 1 MGNSSIMFLFAAAATGVHSQVQLVQSGAEVKKPGASVKLSCKASGYTFTSYNHWVKQRP 60
 QY 61 GQRFENWGWINPYNNGNKEPSAKQDRVFTADTSANTAYMELSLRSADTAVVYCARVGP 120
 DB 61 GRLEWIGRIDPSGDTKFNKEKRTKATLVDPKPSVYVNHLSRSLTSADSAVYICTRGL 120
 QY 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
 DB 121 FY---SDYVDYSDYNGQGTIVVSS 143
 RESULT 22
 Q9UL94 PRELIMINARY; PRT; 119 AA.
 AC Q9UL94
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR HSP; P01772; 2FB4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; IGV.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 1
 SQ SEQUENCE 124 AA; 13580 MW; 1BAAACED96ACD2A2 CRC64;
 Query Match 51.3%; Score 406.5; DB 4; Length 124;
 Best Local Similarity 62.6%; Pred. No. 3.2e-35;
 Matches 82; Conservative 13; Mismatches 25; Indels 11; Gaps 2;
 QY 20 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPQRFENWGWINPYNNGNKEF 79
 DB 1 EVQLVESGAEVKKPGASVKVSCKASGYTFTSYNHWVRQAPQGLGWGWINPNSWTTNY 60
 QY 80 SAKFQDRVFTADTSANTAYMELSLRSADTAVVYCARVGPYVSWDDSPQDNYMDVWGK 139
 DB 61 AQKFGQVMTKDTSTISAYMELSLRSDDTAVVYCARGG-----GRGLWFDPMQGG 112
 QY 140 TTVIVSS 146
 DB 113 TLTVVSS 119
 RESULT 23
 Q9UL92 PRELIMINARY; PRT; 124 AA.
 AC Q9UL92
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR HSP; P01772; 2FB4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; IGV.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 1
 SQ SEQUENCE 124 AA; 13580 MW; 1BAAACED96ACD2A2 CRC64;
 Query Match 51.3%; Score 406.5; DB 4; Length 124;
 Best Local Similarity 62.6%; Pred. No. 3.2e-35;
 Matches 82; Conservative 13; Mismatches 25; Indels 11; Gaps 2;
 QY 20 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPQRFENWGWINPYNNGNKEF 79
 DB 1 EVQLVESGAEVKKPGASVKVSCKASGYTFTSYNHWVRQAPQGLGWGWINPNSWTTNY 60
 QY 80 SAKFQDRVFTADTSANTAYMELSLRSADTAVVYCARVGPYVSWDDSPQDNYMDV 135
 DB 61 AQKFGQVMTKDTSTISAYMELSLRSDDTAVVYCARGLVWVPAAFS-----RFDY 113
 QY 136 WGKGTIVVSS 146
 DB 114 WQGTIVVSS 124
 RESULT 24
 Q91WR1 PRELIMINARY; PRT; 498 AA.
 ID Q91WR1
 AC Q91WR1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.

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GN IGH-VJ558 OR AI933585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL EMBL; BC013539; AAH13539.1; -.
DR EMBL; BC013539; AAH13539.1; -.
DR MGI; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match 51.1%; Score 405.5; DB 11; Length 488;
Best Local Similarity 50.3%; Pred. No. 2.2e-34;
Matches 76; Conservative 30; Mismatches 32; Indels 13; Gaps 3;

Qy 1 MEWSWFLFLLSVTTGVHVSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFWVHWVRQAP 60
Db 1 MGWNWIFLLSGTAGIYSEVQLQSQGPVLKPGASVKLSKASGYTIDYYNWKQSH 60

Qy 61 GQFEWGWINPYNKKEFSAKQDRVTFTADTSANTAYMELSLRSADTAVYICARVGP 120
Db 61 GKSLEWIGDINPYNKNGTSYNGKFKGKATLTVDKSSSTAYMQLNLRTSDSAVYICAR-GP 119

Qy 121 -----YSWDDSPQDNYNMDVWGKTTIVSS 146
Db 120 VYISYFSIDRG-----DIWGQTLVTVSA 143

RESULT 25
Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95,
DC 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RA fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035019; AAD56255.1; -.
DR HSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON TER 1
FT NON TER 125
SQ SEQUENCE 125 AA; 13516 MW; OD3CD5C232488EAC CRC64;

Query Match 50.9%; Score 404; DB 4; Length 125;
Best Local Similarity 62.2%; Pred. No. 5.9e-35;

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Matches 79; Conservative 15; Mismatches 31; Indels 2; Gaps 1;

Qy 20 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFWVHWVRQAPGQRFPEWGWINPYNKKEF 79
Db 1 EYQLVESGAEVKKPGASVKVSQASGYTFTGYVHWVRQAPGQGLEWVGWVNPNSGGTNY 60
[1]
Qy 80 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPVSWDDSPQDNYNMDVWGK 139
Db 61 AQKVQGRVTMTDITISTAYMELSLRSADTAVYICARSGGGRIAAAGDAF--DIWGQ 118

Qy 140 TTVIVSS 146
Db 119 TMTVSS 125

RESULT 26
Q7TMT6 PRELIMINARY; PRT; 614 AA.
AC Q7TMT6,
DC 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faley J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053409; AAH53409.1; -.
KW Hypothetical protein.
SQ SEQUENCE 614 AA; 67746 MW; 839BAF38D124F89 CRC64;

Query Match 50.4%; Score 400; DB 11; Length 614;
Best Local Similarity 53.4%; Pred. No. 1.1e-33;
Matches 78; Conservative 25; Mismatches 35; Indels 8; Gaps 2;

Qy 1 MEWSWFLFLLSVTTGVHVSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFWVHWVRQAP 60
Db 1 MEWPCIFLLSVTTGVHVSQVQLQSQGPVLKPGASVKLSKASGYAFSSWMVWKQRP 60
[1]
Qy 61 GQFEWGWINPYNKKEFSAKQDRVTFTADTSANTAYMELSLRSADTAVYICARVGP 120
Db 61 CKGLEWIGRVYVPGDITNYNGKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCAR--D 118

Qy 121 YSWDDSPQDNYNMDVWGKTTIVSS 146

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Db      119 YG-----SSYRFAYWCGGLTVTVSA 138
                                         :||:||| |||
RESULT 27
Q96DKO PRELIMINARY; PRT; 496 AA.
AC Q96DKO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ25298.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Gastric mucosa;
RA Ishibashi T., Kanehori K., Yoeida M., Watanabe S., Ishida S., Ono Y.,
RA Hctuba T., Hirakawa S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yanashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura A.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Negai K., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR ENML; AK058027; BAB71633.1; --
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_4.
DR SMART; SMC0406; IGv. 1.
DR PROSITE; PS00835; IG_LIKE. 4.
DR PROSITE; PS00290; IG_MHC. 1.
KW Hypothetical protein.
SQ SEQUENCE 496 AA; 53532 MW; C72EE1E247C86FED CRC64;
Query Match 50.3%; Score 398.5; DB 4; Length 496;
Best Local Similarity 54.8%; Pred. No. 1.2e-33;
Matches 80; Conservative 15; Mismatches 48; Indels 3; Gaps 1;

Qy 1 MENSWSVLFSLSVTTGVHSHQVLVSQAEVKKPGASVKVSCQASGYRFSNFVIHWVRQAP 60
Db 1 MDWTRELFVVAAATVTGVQSQVHLVQSGAELKMPGSSVKVSKASKANMFRSYFTWVRQAP 60
Qy 61 GORPEWGWINPYNGNKFEAKFDORTFTADTSANTAYMELSRLSADTAVYCARVGP 120
Db 61 GGQLWGGLIPNGAPNYAQNFQDVRTISADDSTTVYMELTSITFEDTAFCGRGLT 120
Qy 121 YSWDDSPQDNMYMDVGKGTTIVSS 146
Db 121 VYGSGS---YYLQHWGGGLTVTVSS 143

RESULT 28
O95978 PRELIMINARY; PRT; 157 AA.
AC O95978;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH1 protein precursor (fragment).
GN VH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,
RA Bohlen H., Diehl V., Wolf J.;
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RT	"Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a									
RT	patient with mixed cellularity Hodgkin's disease is associated with									
RT	somatic mutations within the untranslated regions of rearranged and									
RT	class switch recombinated Ig genes."									
RL	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.									
DR	EMBL:	AU005570;	CAA06599.1;	-;						
DR	HSSP:	P01772;	2FB4							
DR	InterPro:	IPR007110;	Ig-like.							
DR	InterPro:	IPR003596;	Ig_V.							
DR	Pfam:	PF00047;	Ig; 1.							
DR	SMART:	SM00406;	IGV; 1.							
DR	PROSITE:	PS50835;	IG_LIKE; 1.							
DR	Signal.									
PT	SIGNAL	1	21	POTENTIAL.						
PT	NON TER	157	157							
SQ	SEQUENCE	157 AA;	17304 MW;	86985EDDA84D8EB5	CRC64;					
Query Match 50.2%; Score 398; DB 4; Length 157;										
Best Local Similarity 54.8%; Pred. No. 3.4e-34;										
Matches 80; Conservative 16; Mismatches 44; Indels 6; Gaps 2										
Qy	1	MEWSWFLPFLSVTTGVHSHQVQLVQSGAEVKKPKASVKVSCQAGYRFSNFIHWVRQAP	60							
Db	1	MDMTWRVFCLLAAVAPGVHSHQVQLVQSGAEIKRPQASVKVCKTSGVFTSYIIHWVRQPR	60							
Qy	61	GQRFEMGMWNPYNGKFFSAKFDQRTFTADTSANTAYMELRSLRSADTAVTYCARVGP	120							
Db	61	GQGLEWGGIGFGVSGITWCAEKFGRLTMTNTSTTTVMYELSLRLAFEDTAVVFCRGG-	119							
Qy	121	YSWDSPQDNYMVDVWGKGTIVVSS	146							
Db	120	-RW- ---RSGNYNGHWGGGTFTVSS	140							
RESULT 29										
Q8R3H6	Q8R3H6	PRELIMINARY;	PRT;	474 AA.						
ID	Q8R3H6	AC								
DT	01-JUN-2002 (TrEMBLrel. 21, Created)									
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)									
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)									
DE	Hypothetical protein.									
GN	AU044919.									
OS	Mus musculus (Mouse).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.									
EN	NCBI_TaxId:10090;									
FN	[1]									
RP	SEQUENCE FROM N.A.									
RA	Strausberg R.;									
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.									
DR	EMBL:	BC025447;	AAH25447.1;	-;						
DR	MGI:	2144967;	AU044919.							
GO:	GO:0005489;	F-electron transporter activity;	IEA.							
GO:	GO:0006118;	P-electron transport;	IEA.							
DR	InterPro:	IPR000345;	CysC heme_BS.							
DR	InterPro:	IPR007110;	Ig-like.							
DR	InterPro:	IPR003006;	Ig_MHC.							
DR	InterPro:	IPR003596;	Ig_V.							
DR	Pfam:	PF00047;	Ig; 3.							
DR	SMART:	SM00406;	IGV; 1.							
DR	PROSITE:	PS00190;	CYTCHROME C; 1.							
DR	PROSITE:	PS50835;	IG_LIKE; 4.							
DR	PROSITE:	PS00290;	IG_MHC; 1.							
KW	Hypothetical protein.									
SQ	SEQUENCE	474 AA;	51748 MW;	8608B57C6CD2874A	CRC64;					
Query Match 50.2%; Score 398; DB 11; Length 474;										
Best Local Similarity 54.1%; Pred No. 1.3e-33;										
Matches 79; Conservative 24; Mismatches 35; Indels 8; Gaps 2										
Qy	1	MEWSWFLPFLSVTTGVHSHQVQLVQSGAEVKKPKASVKVSCQAGYRFSNFIHWVRQAP	60							

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Db      1  MWEPICILLPLSVTEGVHSQVQLIQSGPELVKPGASVKISCRASGVYAFSKSMNWVWVRRP 60
QY      61  GQRFWMGWINPYNGKNKFSAKFQDRVFTTADTSAANTAYMELSLRSADTAVYICARVGP 120
Db      61  KGLEWIGRIPEGDDTHYSYSGFKAKLTADKSSVTAFTQLTSLTSEDVAVYFCAR--- 117
QY      121  YSWDDSPQDNIYYMDVWGKGTTIVVSS 146
Db      118  ---DSDYGDYF-PDWGOGAVTVSS 138

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RESULT 30

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Q991A6 PRELIMINARY; PRT; 484 AA.
ID Q991A6
AC Q991A6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE DT
DE Hypothetical protein.
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003495; AAH03495.1; -.
DR FIR; F33932; F33932.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00C04; Ig. 4.
DR SMART; SM00406; IGV. 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
DE Hypothetical protein.
KW
SQ SEQUENCE 484 AA; 52567 MW; 8EAFA4F9BCF582FA CRC64;

```

Search completed: August 26, 2004, 13:39:24
Job time : 39.3926 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:33:27 ; Search time 8.65185 Seconds
(without alignments)
878.684 Million cell updates/sec

Title: US-10-016-986-155
Perfect score: 793
Sequence: 1 MEWSWFLPFLSVTTGVHSQ.....PQDNYMDVMGKTTIVSS 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt 42.1*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	459.5	57.9	147	1	HVIC_HUMAN
2	433	54.6	117	1	HVIC_HUMAN
3	431	54.4	117	1	HVIC_HUMAN
4	423	53.3	140	1	HVIC_MOUSE
5	408.5	51.5	139	1	HVIC_MOUSE
6	402	50.7	117	1	HVIC_MOUSE
7	391.5	49.4	137	1	HVIC_MOUSE
8	389	49.1	138	1	HVIC_MOUSE
9	383	48.3	117	1	HVIC_MOUSE
10	378.5	47.7	120	1	HVIC_HUMAN
11	375	47.3	117	1	HVIC_MOUSE
12	374	47.2	136	1	HVIC_MOUSE
13	370	46.7	117	1	HVIC_MOUSE
14	362	45.6	120	1	HVIC_MOUSE
15	360	45.4	117	1	HVIC_MOUSE
16	360	45.4	117	1	HVIC_MOUSE
17	357.5	45.1	120	1	HVIC_MOUSE
18	355	44.8	117	1	HVIC_MOUSE
19	354	44.6	117	1	HVIC_MOUSE
20	352	44.4	117	1	HVIC_MOUSE
21	351.5	44.3	118	1	HVIC_MOUSE
22	347	43.8	117	1	HVIC_MOUSE
23	341	43.0	117	1	HVIC_HUMAN
24	339	42.7	125	1	HVIC_HUMAN
25	328.5	41.4	114	1	HVIC_MOUSE
26	321	40.5	121	1	HVIC_MOUSE
27	316.5	39.9	136	1	HVIC_MOUSE
28	311.5	39.3	119	1	HVIC_MOUSE
29	302.5	38.1	144	1	HVIC_MOUSE
30	298.5	37.6	124	1	HVIC_HUMAN
31	296.5	37.4	122	1	HVIC_HUMAN
32	293	36.9	146	1	HVIC_HUMAN
33	292	36.8	119	1	HVIC_HUMAN

34	291	36.7	121	1	HVIC_HUMAN
35	290.5	36.6	122	1	HVIC_HUMAN
36	290.5	36.6	124	1	HVIC_HUMAN
37	289.5	36.5	122	1	HVIC_MOUSE
38	289	36.4	123	1	HVIC_MOUSE
39	288	36.3	123	1	HVIC_MOUSE
40	286.5	36.1	122	1	HVIC_MOUSE
41	285	35.9	123	1	HVIC_MOUSE
42	284	35.8	123	1	HVIC_MOUSE
43	283	35.7	118	1	HVIC_MOUSE
44	283	35.7	123	1	HVIC_MOUSE
45	283	35.7	123	1	HVIC_MOUSE
46	282.5	35.6	119	1	HVIC_MOUSE
47	282	35.6	137	1	HVIC_MOUSE
48	281	35.4	117	1	HVIC_HUMAN
49	279.5	35.2	119	1	HVIC_MOUSE
50	277.5	35.0	119	1	HVIC_HUMAN
51	276	34.8	117	1	HVIC_MOUSE
52	275.5	34.7	126	1	HVIC_MOUSE
53	275	34.7	115	1	HVIC_HUMAN
54	273.5	34.5	122	1	HVIC_HUMAN
55	272	34.3	117	1	HVIC_MOUSE
56	271.5	34.2	116	1	HVIC_MOUSE
57	270.5	34.1	117	1	HVIC_MOUSE
58	270	34.0	142	1	HVIC_MOUSE
59	266.5	33.6	117	1	HVIC_MOUSE
60	265	33.4	144	1	HVIC_MOUSE
61	262	33.0	116	1	HVIC_MOUSE
62	261	32.9	119	1	HVIC_HUMAN
63	260.5	32.8	116	1	HVIC_HUMAN
64	259.5	32.7	120	1	HVIC_HUMAN
65	259	32.7	120	1	HVIC_HUMAN
66	258	32.5	117	1	HVIC_MOUSE
67	256.5	32.3	114	1	HVIC_HUMAN
68	255.5	32.2	115	1	HVIC_HUMAN
69	255	32.2	115	1	HVIC_HUMAN
70	254.5	32.1	118	1	HVIC_HUMAN
71	254	32.0	116	1	HVIC_HUMAN
72	253.5	32.0	117	1	HVIC_HUMAN
73	253	31.9	117	1	HVIC_MOUSE
74	251.5	31.7	119	1	HVIC_MOUSE
75	250	31.5	116	1	HVIC_MOUSE
76	249.5	31.5	117	1	HVIC_MOUSE
77	248	31.3	116	1	HVIC_MOUSE
78	247.5	31.2	114	1	HVIC_MOUSE
79	247.5	31.2	119	1	HVIC_MOUSE
80	247	31.1	117	1	HVIC_HUMAN
81	244	30.8	116	1	HVIC_MOUSE
82	244	30.8	117	1	HVIC_MOUSE
83	244	30.8	117	1	HVIC_MOUSE
84	242	30.5	117	1	HVIC_MOUSE
85	242	30.5	117	1	HVIC_MOUSE
86	240	30.3	98	1	HVIC_MOUSE
87	240	30.3	129	1	HVIC_MOUSE
88	239	30.1	135	1	HVIC_MOUSE
89	237.5	29.9	111	1	HVIC_MOUSE
90	236.5	29.8	97	1	HVIC_MOUSE
91	235	29.6	117	1	HVIC_MOUSE
92	233.5	29.4	116	1	HVIC_MOUSE
93	229	28.9	113	1	HVIC_MOUSE
94	229	28.9	115	1	HVIC_MOUSE
95	225	28.4	115	1	HVIC_MOUSE
96	224.5	28.3	117	1	HVIC_MOUSE
97	224	28.2	113	1	HVIC_MOUSE
98	223.5	28.2	117	1	HVIC_MOUSE
99	223	28.1	113	1	HVIC_MOUSE
100	222	28.0	113	1	HVIC_MOUSE

ALIGNMENTS

RESULT 1

```

HV1C_HUMAN
ID HV1C_HUMAN STANDARD; PRT; 147 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo I.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBO J. 7:1047-1051(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
DR EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVH035.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117
FT SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
Query Match 54.6%; Score 433; DB 1; Length 117;
Best Local Similarity 68.4%; Pred. No. 2.1e-37;
Matches 80; Conservative 12; Mismatches 25; Indels 0; Gaps 0;
QY 1 MEWSVFLFFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 MDWTWRIILFLVAATGAHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
QY 61 GQFEWGWINPYNKKEFSAKQDRVTFTADTSANTAYMELSLRSADTAVVYCAR 117
Db 61 GQGLEWGWINPYNKGGTNYAOKFGQRTVTRDTSISITAYMELSLRSDDITVYVYCAR 117
RESULT 3
HV1C_HUMAN
ID HV1C_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups."
RT Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
QY 1 MEWSVFLFFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 MDWTWRIILFLVAATGAHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
QY 61 GQFEWGWINPYNKKEFSAKQDRVTFTADTSANTAYMELSLRSADTAVVYCAR 117
Db 61 GQGLEWGWINPYNKGGTNYAOKFGQRTVTRDTSISITAYMELSLRSDDITVYVYCAR 117
RESULT 2
HV1C_HUMAN
ID HV1C_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
QY 121 YSDD--SPQDNYMDVWGKGTIVSS 146
Db 121 F-WSDYNYFDYSYILDVWGQGTIVTSS 147
Query Match 57.9%; Score 459.5; DB 1; Length 147;
Best Local Similarity 58.1%; Pred. No. 5.2e-40;
Matches 86; Conservative 24; Mismatches 35; Indels 3; Gaps 2;
QY 1 MEWSVFLFFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 MDWTWRIILFLVAATGAHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
QY 61 GQFEWGWINPYNKKEFSAKQDRVTFTADTSANTAYMELSLRSADTAVVYCARVGP 120
Db 61 GHGLEWGWINPYNKGGTNYAOKFGQRTVTRDTSISITAYMELSLRSDDITVYVYCARVGP 120
QY 121 YSDD--SPQDNYMDVWGKGTIVSS 146
Db 121 F-WSDYNYFDYSYILDVWGQGTIVTSS 147

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CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00240; AAAS2988.1; -.
CC PIR; A02024; HVHUNG.
CC HSSP; P01772; 2FB4.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; P:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC KW Immunoglobulin V region; Hydrindoma; Signal.
CC FT SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
CC DOMAIN 20 >117 IG-LIKE.
CC NON TER 117
CC SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 54.4%; Score 431; DB 1; Length 117;
Best Local Similarity 58.4%; Pred. No. 3.3e-37;
Matches 80; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

QY 1 MEWSVFLFLSVTTGVHSGVQLVQSGAEVKKFGASVKVSCQASGYRFSNFIHWVRQAP 60
Db 1 MDWTRVFCCLAVAPGAHSGVQLVQSGAEVKKFGASVKVSCQASGYTFSNFIHWVRQAP 60

QY 61 GQFEWMCWNPYNGKNEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYICAR 117
Db 61 GQLEWNGIINPGSGTSYAQKFGQRTVTRDTSTSTVMEJSSLSRSEDATVYICAR 117

RESULT 4
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=92152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess F., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; J00493; AAA38128.1; -.

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DR PIR; A94264; HVMSG7.
DR HSSP; P01810; 2FBD.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hydrindoma; Signal.
FT SIGNAL 1 19
CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
DOMAIN 20 139 IG-LIKE.
NON TER 140
SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 53.3%; Score 423; DB 1; Length 140;
Best Local Similarity 54.8%; Pred. No. 2.7e-36;
Matches 80; Conservative 27; Mismatches 33; Indels 6; Gaps 1;

QY 1 MEWSVFLFLSVTTGVHSGVQLVQSGAEVKKFGASVKVSCQASGYRFSNFIHWVRQAP 60
Db 1 MGWSEIFLFLSVTAGVHSEVQLQSGAEVLRAGSSVKVSCKASGYTFSYGINVWVRQAP 60

QY 61 GQFEWMCWNPYNGKNEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYICARVGP 120
Db 61 GQLEWIGYINPGNGYINYNKFKGKTLTVKSSSTAYMQLRSLTSEDSAVYFCARSHY 120

QY 121 YSWDDSPQDNYMDVWVGKGTIVVSS 146
Db 121 YG-----GSYDFYWGQGTPLTVSS 140

RESULT 5
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00529; AAA38170.1; -.
CC PIR; A30809; MHXS18.
CC PDB; 1A6U; 27-MAY-98.
CC PDB; 1A6W; 15-JUL-98.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.

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KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4ED0C9F465 CRC64;

Query Match 51.58; Score 408.5; DB 1; Length 139;
Best Local Similarity 52.18; Pred. No. 8e-35;
Matches 76; Conservative 26; Mismatches 37; Indels 7; Gaps 1;

QY 1 MWSWFLFFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MGWSIMFLAATATGVSQVQLQPGAEELVKPGASVLSCKASGYTFTSYMMHWVKQRP 60
QY 61 GQRFEMGWNPNGNKEFSAKQDRVTFADTSANTAYMELSLRSADTAVYVCARVCP 120
DB 61 GRGLEWIGRIDPNSGGTKYKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYVCARDY 120
QY 121 YSWDDSPQDNYMDVWGKGTITVSS 146
DB 121 YG-----SSYFDYWGQGITLVSS 139

RESULT 6
ID HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 108A precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; J00488; AAA38519.1; -.
CC PIR; A02041; HVMS8A.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
CC DOMAIN 20 117 IG-LIKE.
CC FRAMEWORK-1.
CC FRAMEWORK-2.
CC FRAMEWORK-3.
CC D SEGMENT.
CC JH2 SEGMENT.
CC BY SIMILARITY.
CC
CC Query Match 49.4%; Score 391.5; DB 1; Length 137;
CC Best Local Similarity 50.7%; Pred. No. 4.3e-33;
CC Matches 74; Conservative 24; Mismatches 39; Indels 9; Gaps 1;

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FT NON TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 50.7%; Score 402; DB 1; Length 117;
Best Local Similarity 60.7%; Pred. No. 3e-34;
Matches 71; Conservative 21; Mismatches 25; Indels 0; Gaps 0;

QY 1 MWSWFLFFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MGWSWFLFFLSVTTGVHSQVQLVQSGAEVKKPGASVKISCKASGYTFTDYNHWVKQSH 60
QY 61 GQRFEMGWNPNGNKEFSAKQDRVTFADTSANTAYMELSLRSADTAVYVCAR 117
DB 61 GKSLEWIGIYIPYNGTGYNQKFKSKATLTVDNSSLTSEDSAVYVCAR 117

RESULT 7
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
CC (NPB ANTIBODIES).
CC
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CC
CC EMBL; J00539; AAA38172.1; -.
CC PIR; A02038; G2MS43.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
CC DOMAIN 20 49 FRAMEWORK-1.
CC COMPLEMENTARITY-DETERMINING-1.
CC FRAMEWORK-2.
CC COMPLEMENTARITY-DETERMINING-2.
CC FRAMEWORK-3.
CC D SEGMENT.
CC JH2 SEGMENT.
CC BY SIMILARITY.
CC
CC Query Match 49.4%; Score 391.5; DB 1; Length 137;
CC Best Local Similarity 50.7%; Pred. No. 4.3e-33;
CC Matches 74; Conservative 24; Mismatches 39; Indels 9; Gaps 1;

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QY 1 MEWSWFLFELSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60
Db 1 MGWSCIMFLAATATGATGHSQVQLVQSGAEVKKPGASVKLSCKASGTFSTYLMHWYQRP 60
QY 61 GORFEMWGINPYNGNKEFSQDRVTFTADTSANTAYMELRSLSADTAVVYCARVGP 120
Db 61 GRGLEWIGRIDPNSGGTTYNEHFRSKATLTIDKPSSTAYMQLSSLTSDSAVVCARY-- 118
QY 121 YSWDDSPQDNYNDVWGKGTIVVSS 146
Db 119 -----RLGRYFDYWGQGITLVSS 137

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RESULT 8

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HV48 MOUSE
ID HV48 MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=84248078; PubMed=6429663;
RX Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HWSM77.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 21 49 FRAMEWORK-2.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 58 FRAMEWORK-3.
FT DOMAIN 66 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-4.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-5.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

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Query Match 49.1%; Score 389; DB 1; Length 138;
Best Local Similarity 50.0%; Pred. No. 7.8e-33;
Matches 74; Conservative 25; Mismatches 37; Indels 12; Gaps 2;

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QY 1 MEWSWFLFELSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60
Db 1 MGWSYIILFLVATATDVHSGVQLVQSGAEVKKPGASVKLSCKASGTFSTYLMHWYQRP 60
QY 61 GORFEMWGINPYNGNKEFSQDRVTFTADTSANTAYMELRSLSADTAVVYCARVGP 120
Db 61 GQGLEWIGELNPDGSRNRYNEKPKATLTVDKSSSTAYMQLSSLTPBEFAVVCAR--- 117
QY 121 YSWDDSPQDNY--MDVWGKGTIVVSS 146
Db 118 -----SDGYDFWVWGQGITLVTS 138

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RESULT 9

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HV52 MOUSE
ID HV52 MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=8509340; PubMed=2578321;
RX Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
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CC -----
CC EMBL; M13787; AAA38499.1; -.
DR PIR; A02029; HVMSA1.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

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Query Match 48.3%; Score 383; DB 1; Length 117;
Best Local Similarity 58.1%; Pred. No. 2.7e-32;
Matches 68; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

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QY 1 MEWSWFLFELSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWRQAP 60
Db 1 MGWRWIFLLSGTAGVHCQVQLQSGPELVKPKALTKADKSSSTAYMQLSSLTSENSAVVCAR 60
QY 61 GORFEMWGINPYNGNKEFSQDRVTFTADTSANTAYMELRSLSADTAVVYCAR 117
Db 61 GQGLEWIGWIFPGDGSIKYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVVCAR 117

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RESULT 10

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HV1H HUMAN
ID HV1H HUMAN STANDARD; PRT; 120 AA.
AC P80421;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-I region DOT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclinal
RL immunoglobulins."
RL Eur. J. Biochem. 228:886-893(1995).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP: P01772; 2PB4
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT DISULFID 22 95 BY SIMILARITY.
FT NON TER 120 120
SQ SEQUENCE 120 AA; 13272 MW; F1307FD253A782F1 CRC64;

Query Match 47.78; Score 378.5; DB 1; Length 120;
Best Local Similarity 62.78; Pred. No. 7.9e-32;
Matches 79; Conservative 13; Mismatches 27; Indels 7; Gaps 3;

Qy 21 VQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEGWGMINPYNGKERS 80
Db 2 VQLVQSGVERKPGASVRIKCKASGAFENYIHWVRQAPGLGLEWVGFNPVAGAVS-S 60

Qy 81 AKFQDRVTFADTSANTAYMELSLRSADTAVYYCARVGVSDSDPQNYMDVWGKGT 140
Db 61 EKFRDLVMSDTSANTVSMQLNLSRSDTGRYFCARV---SYDFS---QYGMVDVWGQGT 114

Qy 141 TVIVSS 146
Db 115 TVIVSS 120

RESULT 11
HV09 MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DE 15-JUN-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6783376;
RA Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR: D90809; HVMS61.
DR HSP: P01810; 2PB1.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.

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FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 47.38; Score 375; DB 1; Length 117;
Best Local Similarity 57.38; Pred. No. 1.8e-31;
Matches 67; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MEWSWVFLFSLVTTGVHSHQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
Db 1 MGWSCIMFLAATATGVHSHQVQLVQSGAEVKKPGASVKLSCKASGYFTSYVHWVRQAP 60

Qy 61 GQFPEWGMWNPYNGKERSAKFQDRVTFADTSANTAYMELSLRSADTAVYYCAR 117
Db 61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLVDTSSSTAYMQLHSLTSEDSAVYYCAR 117

RESULT 12
HV15 MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT by two adjacent CH genes."
RT Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC
CC EMBL; J00494; AAA38130.1; -.
CC PIR; A02042; HVMSB1.
CC HSP: P01772; 2PB4.
CC InterPro: IPR007110; IG-like.
CC InterPro: IPR003596; IG_v.
CC Pfam: PF00047; ig; 1.
CC SMART: SM00406; Igv; 1.
CC PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT DOMAIN 20 135 IG-LIKE.
FT NON TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 47.28; Score 374; DB 1; Length 136;
Best Local Similarity 47.98; Pred. No. 2.6e-31;
Matches 70; Conservative 26; Mismatches 40; Indels 10; Gaps 2;

Qy 1 MEWSWVFLFSLVTTGVHSHQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60

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Db 1 MGWSCIFFFLVATGATGHSQVQLQSGPEVVRPGVSKICKSGYTFDTYAMHWKQSH 60
QY 61 GQFEFWGWINPYNKGKFAKQDRVTFADTSANTAYMELSLRSADTAVVYCARVGP 120
Db 61 AKSLEWIGVISTYNGTSYNQKFKGATMTVDKSSSTVHVELARLTSEDSANLYCARY-- 118
QY 121 YSWDDSPQDNYMDVWGKGTFTVSS 146
Db 119 -----YGNYP-DYWGQGTTLVSS 136

RESULT 13
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; A02030; HVMS23.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 46.7%; Score 370; DB 1; Length 117;
Best Local Similarity 57.3%; Pred. No. 5.7e-31;
Matches 67; Conservative 20; Mismatches 30; Indels 0; Gaps 0;

QY 1 MWSWFLFFLSVTGHSQVQLQSGAEVKPKGASVKVSCQASGYRFSNFIHWRQAP 60
Db 1 MGWSCILFLVAANGVHSQVQLQPGTELVKFGASVKLSCKASGYTFSTYWMHWKQRP 60
QY 61 GQFEFWGWINPYNKGKFAKQDRVTFADTSANTAYMELSLRSADTAVVYCAR 117
Db 61 GQGLEWIGNPONGGTYNNEKFSKTLTVDKSSSTAVTQLSSLTSEDSAVVYCAR 117

RESULT 14
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
```

```
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 45.6%; Score 362; DB 1; Length 120;
Best Local Similarity 54.0%; Pred. No. 3.9e-30;
Matches 68; Conservative 25; Mismatches 27; Indels 6; Gaps 1;

QY 21 VOLVSGAEVKPKGASVKVSCQASGYRFSNFIHWRQAPQRFWMGWINPYNKGKFS 80
Db 1 VOLQSGAELVRAGSSVSKASGYTFSTYGINWVKQPCQGLEWIGYINPGNGYTKYN 60
QY 81 AKFQDRVTFADTSANTAYMELSLRSADTAVVYCARVGPYSWDDSPQDNYMDVWGKGT 140
Db 61 EKFKGKTLTVDKSSSTAYMQLSLTSEDSAVVYCARSVYVG-----GSYFYFDWGQGT 114
QY 141 TVIVSS 146
Db 115 TLTVSS 120

RESULT 15
HV06_MOUSE
ID HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; A02032; HVMS02.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
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CC EMBL; J00536; AAA38605.1; -.
CC PIR; AC2031; 2FEJ.
CC HSSP; P01810; 2FEJ.
CC MGD; MGI:96486; Igh-VJ558.
CC DR InterPro; IPR007110; Igh-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG LIKE; 1.
CC KW Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
CC FT DOMAIN 20 49 FRAMEWORK-1.
CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 55 68 FRAMEWORK-2.
CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 86 117 FRAMEWORK-3.
CC FT DISULFID 41 115 BY SIMILARITY.
CC FT NON TPR 117 117
CC SQ SEQUENCE 117 AA; 427C861C53975EDC CRC64;
Query Match 44.6%; Score 354; DB 1; Length 117;
Best Local Similarity 54.7%; Pred. No. 2.5e-29;
Matches 64; Conservative 23; Mismatches 30; Indels 0; Gaps 0;
Qy 1 MENSWVFLFSLVTGVHSGVOLVSGAELVKKSGASVKVSCQASGYRFSNFVHVYQAP 60
Db 1 MGWSCIILFVATGVHSGVQVQQPGLVLRPGSSVKLSCKASGYTFTSYWMDWKQRP 60
Qy 61 GQRFPMGWNIPYNGNKESAKFDQRTVTFADTASANTAYNELSLRSADTAVYYCAR 117
Db 61 GQGLEWIGNIYPSDSETHYNKQKFKRATLIVDKSSSTAYNQLSLSLTSDESAVYYCAR 117
RESULT 20
HV49 MOUSE
ID HV49 MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DR Ig heavy chain V region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
RL Cell 40:271-281 (1985).
CC
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CC or send an email to license@lsb-sib.ch).
CC
CC EMBL; M13786; AAA38506.1; -.
CC PIR; A02035; MEMSB4.
CC HSSP; P01810; 2FEJ.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG LIKE; 1.
CC KW Immunoglobulin V region; Signal.
CC

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FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 59 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match
Best Local Similarity 53.8%; Score 352; DB 1; Length 117;
Matches 63; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 1 MEWSWVFLFFLSVTGHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MGWSCIMFLAATATGVHSPVQLQPGAEVLKPGASVKLSKASGYTFTSYMHWVKQRP 60

QY 61 GQRFEMWGINPYNGKPEKSAKQDRVFTADTSANTAYMELRLSADTAVYYCAR 117
DB 61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYYCTR 117

RESULT 21
HVSI_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Sikevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotype) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02040; MMS38.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS00835; IG LIKE; 1.
DR KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104
FT DOMAIN 105 118
FT DISULFID 22 96
FT NON TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEEAC762A018 CRC64;

Query Match
Best Local Similarity 44.3%; Score 351.5; DB 1; Length 118;
Matches 68; Conservative 21; Mismatches 29; Indels 9; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFEMWGINPYNGKPEF 79
DB 1 EVQLQSGPELVKPGASVKISCKASGYTFTDYNNWYKQSHGKSLKLEWIGIDINPNNGTGY 60

QY 80 SAKFQDRVFTADTSANTAYMELRLSADTAVYYCARVPYSDSDSPQDNYMDVMVGKG 139
DB 61 NQKFKGATLTVDKSSATYMLRLSLTSEDSAVYYCAR--GYGYDP-----FDVWGIG 111

140 TTVTVSS 146
112 TTVTVSS 118

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RESULT 22
HV10_MOUSE STANDARD; PRT; 117 AA.
ID HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain V region 145 precursor.
OS IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6780376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC -----
CC EMBL: J00333; AAA38602.1; -
CC PIR: C90809; HVMS45.
CC HSSP: P01810; 2PBJ.
CC MGD: MGI:96486; Igh-VJ558.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003596; IG_v.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00406; IG; 1.
CC PROSITE: PS00835; IG LIKE; 1.
CC KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match
Best Local Similarity 43.8%; Score 347; DB 1; Length 117;
Matches 63; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 1 MEWSWVFLFFLSVTGHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MGWSCIMFLAATATGVHSPVQLQPGAEVLKPGASVKLSKASGYTFTSYMHWVKQRP 60

QY 61 GQRFEMWGINPYNGKPEKSAKQDRVFTADTSANTAYMELRLSADTAVYYCAR 117
DB 61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYYCAR 117

RESULT 23
HV1A_HUMAN STANDARD; PRT; 117 AA.
ID HV1A_HUMAN
AC P01742;
DT 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gotlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RA "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RA "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90563; GIHUEU.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12472 MW; 99D60ADAEBD52818 CRC64;

Query Match 43.0%; Score 341; DB 1; Length 117;
Best Local Similarity 60.9%; Pred. No. 5.3e-28;
Matches 78; Conservative 7; Mismatches 31; Indels 12; Gaps 3;

QY 20 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGMINPYNGNKEF 79
DB 1 QVQLVQSGAEVKKPGSSVKVSCKASGCTFSRSALINVRQAPGQGLEWMGIVPMFGPPNY 60
QY 80 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYYMDVWGK 138
DB 61 AQRFGQRTTADSTNTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYYMDVWGK 138
QY 139 GTTVIVSS 146
DB 110 GGLVTWSS 117

RESULT 24
HV1F HUMAN STANDARD; PRT; 125 AA.
AC P06326;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region Mot.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

RX MEDLINE=86203277; PubMed=3084950;
RA Kojima M., Koide T., Odani S., Ono T.;
RT "Amino acid sequence of the variable region of heavy chain in
RT immunoglobulin (Mot) having unusual papain cleavage sites.";
RL Mol. Immunol. 23:169-174(1986).
DR PIR; A02025; HVHUMO.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT MOD RES 99 107 D SEGMENT.
FT DISULFID 108 125 J SEGMENT.
FT NON TER 122 96 BY SIMILARITY.
FT NON TER 125 125
SQ SEQUENCE 125 AA; 13579 MW; F4C4285D6DF0C8EA CRC64;

Query Match 42.7%; Score 339; DB 1; Length 125;
Best Local Similarity 52.8%; Pred. No. 9.1e-28;
Matches 67; Conservative 19; Mismatches 39; Indels 2; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAPGQRFPMWGMINPYNGNKEF 79
DB 1 QVQLVQSGAEVKKPGSSVKVSCKASGCTFSRSALINVRQAPGQGLEWMVAVHPSDRTTY 60
QY 80 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYYMDVWGK 139
DB 61 GPRSQARFTVTRDSSTTVYMELTALISADTAIVYICARGAHYS--DTDDSGTSLGPMQGG 118
QY 140 TTVIVSS 146
DB 119 TLLIVSS 125

RESULT 25
HV00 MOUSE STANDARD; PRT; 114 AA.
ID HV00 MOUSE
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region (Anti-arsonate antibody).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=79195438; PubMed=1095336;
RA Capra J.D., Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idiotype.";
RL J. Immunol. 123:279-284(1979).
CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGGL SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02022; GIMGAA.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

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KW Immunoglobulin V region.
FT DOMAIN 1 106 IG-LIKE.
FT NON TER 114 114
SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A69F4BE CRC64;

Query Match 41.4%; Score 328.5; DB 1; Length 114;
Best Local Similarity 54.8%; Pred. No. 9.7e-27;
Matches 68; Conservative 19; Mismatches 26; Indels 11; Gaps 3;

QY 20 QVQLVQSGAEVKKPGASVKVSQCAASGYRFSNFIHVVQRAPGQRFVWGMGWINPYNGKKEP 79
DB 1 EQVQQSGAEVLRGSSVKVSKCATGTFSSYELVWVRAPGGGLDLGIYSSSSAYPNY 60

QY 80 SAKFQDRVTFTADTSANTAYMELRSADTAVYICA-RVGPYSWDSPODNYMDVWGK 138
DB 61 AQKFGQVRITADESTNTAYMELSSLRSEDYAVYFCARV-----ISRYFDWGQ 110

QY 139 GTTV 142
DB 111 GTLV 114

RESULT 26
HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. PubMed=6253904;
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601 (1980).
[2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840 (1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; A93708; GVM511.
DR PIR; A93708; GVM511.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AF3BC5ED0BF CRC64;

Query Match 40.5%; Score 321; DB 1; Length 121;
Best Local Similarity 49.6%; Pred. No. 6.1e-26;
Matches 63; Conservative 26; Mismatches 32; Indels 6; Gaps 3;

QY 20 QVQLVQSGAEVKKPGASVKVSQCAASGYRFSNFIHVVQRAPGQRFVWGMGWINPYNGKKEP 79
DB 1 EAQVQQSGAEVLRGTSVKLSCKAAGTFYNYIGWVKERPGHGLWIGDIYPCGGFTNY 60

QY 80 SAKFQDRVTFTADTSANTAYMELRSADTAVYICARVGPYSWDSPODNYMDVWGK 139
DB 61 NDNLKGRATLTADTSSTAVYIQLSSLTSDSAIYHCAR-GIY-YNSSP-----YFDSWGQ 114

QY 140 TTVIVSS 146

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DB 115 TTVVSS 121

RESULT 27
HV16_MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. PubMed=6788376;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637 (1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RN Nature 265:299-304 (1977).
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DR EMBL; J00522; A015290.1; -.
DR PIR; E90809; G1MS21.
DR PDB; 1IGC; O3-JUN-95.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT NON TER 1 16
FT SIGNAL <1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 39.9%; Score 316.5; DB 1; Length 136;
Best Local Similarity 43.9%; Pred. No. 2e-25;
Matches 61; Conservative 27; Mismatches 44; Indels 7; Gaps 1;

QY 8 LFFLVTTGVHSQVLQVSGAEVKKPGASVKVSQCAASGYRFSNFIHVVQRAPGQRFVW 67
DB 5 VFLVILKGVQCDVQLVESGGGLVQPGSRKLSCAASGFTFSFGMHWVQAPKGLWV 64

QY 68 GWINPYNGKFSKAFQDRVTFTADTSANTAYMELRSADTAVYICARVGPYSWDS 127
DB 65 AVTSSGSSTLHYADTVKGRFTISRDNPNKTLFQMTSLRSDTAVYICARWNPY---- 120

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QY 128 QDNYMDVWGKGTIVVSS 146
DB 121 ---YMDYWGQGTIVVSS 136

RESULT 28
HV28_MOUSE STANDARD; PRT; 119 AA.
AC P01808;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region T601.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79233895; PubMed=111245;
RA RAO D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions."
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02078; AVMST6.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR DOMAIN 1 112 IG-LIKE.
FT NON_TER 119 119
FT SEQUENCE 119 AA; 13169 MW; BC38CC84E6EA00E8 CRC64;

Query Match 39.3%; Score 311.5; DB 1; Length 119;
Best Local Similarity 44.9%; Pred. No. 5.6e-25;
Matches 57; Conservative 26; Mismatches 35; Indels 9; Gaps 1;

QY 20 QVQVSGAEVKPGASVKVSQASGYRFSNFIHVRQAPGQRFWMGWINPYNKKEF 79
DB 1 EVKLSEGGGLVPGGSLKLSCAASGDFSRYMWSVRQAPGKLEWIGEINPDSSTINY 60
QY 80 SAKFQDRVTFDTASANTAYMELRSADTAVYCARVGPYSWDDSPQDNYMDVWGK 139
DB 61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYCARLGYG-----YFDVWGAG 111
QY 140 TTVIVSS 146
DB 112 TTVTVSS 118

RESULT 29
HV26_MOUSE STANDARD; PRT; 144 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region M167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93358330; PubMed=6101209;

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RA Kim S., Davis M., Sinn E., Patten P., Hood L.;
RT "Antibody diversity: somatic hypermutation of rearranged VH genes."
RN Cell 27:573-581(1981).
RP SEQUENCE OF 20-142.
RX MEDLINE=7622762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
RT phosphorylcholine-binding proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS PHOSPHORYLCHOLINE.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00516; AAC18867.2; ALT_TERM.
DR PIR; A90818; AVMS67.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION M167.
FT DOMAIN 20 133 IG-LIKE.
FT CONFLICT 125 125 N -> D (IN REF. 2).
FT NON_TER 144 144
FT SEQUENCE 144 AA; 16219 MW; BECB4A2C956CF769 CRC64;

Query Match 38.1%; Score 302.5; DB 1; Length 144;
Best Local Similarity 40.9%; Pred. No. 5.8e-24;
Matches 61; Conservative 31; Mismatches 44; Indels 13; Gaps 5;

QY 3 W-SWVFLPFLSVTTGVISQVQLVSGAEVKPGASVKVSQASGYRFSNFIHVRQAPG 61
DB 4 WLNWFL--LTLTGLIQCEVKVSGGLVQPGSLKLSCATSGFTFSDFYMEVWVROTPG 61
QY 62 QRFWM--GWINPYNKKEFSAKFQDRVTFDTASANTAYMELRSADTAVYCARVG 119
DB 62 KRLWIAASRSKADHYRTEYSASVKGRTVSRDTSQSVLYLQWNALEADTATYYCTRDA 121
QY 120 PYSWDDSPQDNY--YMDVWGKGTIVVSS 146
DB 122 DYG-----NSYFGYFDVWGAGTTTVSS 144

RESULT 30
HV1E_HUMAN STANDARD; PRT; 124 AA.
AC P01761;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82045599; PubMed=7028111;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of heavy chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa

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RT group.";
RL Biochemistry 20:5822-5830(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02044; MHUS1.
DR HSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 124 124
SQ SEQUENCE 124 AA; 13732 MW; 62CED4573BDEF59F CRC64;

Query Match 37.6%; Score 298.5; DB 1; Length 124;
Best Local Similarity 51.1%; Pred. No. 1.2e-23;
Matches 67; Conservative 16; Mismatches 35; Indels 13; Gaps 5;

Qy 20 QVQLVQSGAEVKKPGASVKYSQASGYRPSNFIHWVRQAPGQRFWMG----WINPYNG 75
Db 1 QVQLVQSGAEVKKPGSSVRVCTSGTSGYTIHWVRQAPGRLWVGSPAKWTDPFQ 60
Qy 76 NKEFSAKQDRVFTADTSANTAYMELSLRSADTAVYICARVGPYSWDDSPQDNYMDV 135
Db 61 ---VYIKW-ERVTVSLKPSFNQAYMELVNLFNEDGAVYICAR----EWKGVNVPF-DY 111
Qy 136 WKGTTIVSS 146
Db 112 WQQGLVTSS 122

Search completed: August 26, 2004, 13:38:02
Job time : 9.65185 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2004, 13:34:32 ; Search time 14.0593 Seconds
(without alignments)
998.912 Million cell updates/sec

Title: US-10-016-986-155
Perfect score: 793
Sequence: 1 MNSWVFLFSLVTTGVHSQ.....PODNYMDVWKGTTIVSS 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

PIR 78.*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	63.2	148	2 S29257	Ig heavy chain V r
2	496	62.5	148	2 S14683	Ig mu chain precursor
3	483	60.9	117	2 S18553	Ig heavy chain V r
4	478.5	60.3	136	2 S38600	Ig heavy chain V r
5	477.5	60.2	135	2 S49530	anti-Sm antibody V
6	475.5	60.0	171	2 S23623	Ig heavy chain V r
7	469	59.1	129	2 S46393	Ig heavy chain V r
8	469	59.1	160	2 PL0105	anti-PR2 erythrocy
9	467	58.9	117	2 S18552	Ig heavy chain V r
10	463	58.4	129	2 S38260	Ig heavy chain V r
11	453	57.1	117	2 S18551	Ig heavy chain V r
12	452.5	57.1	124	2 S19665	Ig heavy chain V r
13	452.5	57.1	143	1 E1HUND	Ig heavy chain pre
14	450	56.7	131	2 S21924	Ig heavy chain V r
15	449	56.6	117	2 S31680	Ig heavy chain V r
16	448.5	56.6	139	2 A27609	Ig heavy chain pre
17	444.5	56.1	474	1 G2MS11	Ig gamma-2b chain
18	443.5	55.9	139	2 FS0024	Ig heavy chain pre
19	442.5	55.8	132	2 S31596	Ig heavy chain V r
20	441	55.6	140	2 PH1482	Ig heavy chain V r
21	438.5	55.3	133	2 PC1155	Ig heavy chain pre
22	437	55.1	123	2 D33548	Ig heavy chain V-1
23	437	55.1	142	2 S19245	Ig heavy chain pre
24	436.5	55.0	118	2 S38265	Ig heavy chain V r
25	433.5	54.7	118	2 PH1666	Ig gamma-2a chain
26	433.5	54.7	469	2 S37483	Ig heavy chain V r
27	433	54.6	117	1 HVHUS3	Ig heavy chain pre
28	433	54.6	133	2 S33548	Ig heavy chain V-1
29	432.5	54.5	137	2 H32513	Ig heavy chain pre

30	432	54.5	142	2 A32483	Ig heavy chain V r
31	431	54.4	117	1 HVHUSG	Ig heavy chain pre
32	430	54.2	140	2 PH1498	Ig heavy chain V r
33	429	54.1	140	2 T01407	Ig heavy chain (my
34	428	54.0	127	2 PH0955	Ig heavy chain V r
35	427	53.8	134	2 S21916	Ig heavy chain V r
36	426.5	53.8	116	2 S31667	Ig heavy chain V r
37	426.5	53.8	135	2 PS0057	Ig heavy chain pre
38	426	53.7	117	2 PT0371	Ig gamma chain pre
39	426	53.7	140	2 PH1484	Ig heavy chain V r
40	425	53.6	111	2 S21925	Ig heavy chain V r
41	425	53.6	135	2 PH1493	Ig heavy chain V r
42	425	53.6	140	2 PH1489	Ig heavy chain V r
43	424	53.5	140	2 PH1488	Ig heavy chain V r
44	423.5	53.4	114	2 PH1667	Ig heavy chain V r
45	423	53.3	140	1 HVMSG7	Ig heavy chain pre
46	421	53.1	136	2 S04576	Ig heavy chain pre
47	420	53.0	122	2 S36271	Ig heavy chain V r
48	420	53.0	140	2 PH1483	Ig heavy chain V r
49	419	52.8	140	2 PH1486	Ig heavy chain V r
50	418.5	52.8	132	2 S46394	Ig heavy chain V r
51	418	52.7	138	2 S21810	Ig heavy chain V r
52	417.5	52.6	150	2 PN0444	Ig heavy chain V r
53	416	52.5	127	2 S34014	Ig heavy chain V r
54	415.5	52.4	126	2 B33548	Ig heavy chain V-1
55	415.5	52.4	132	2 PH0954	Ig heavy chain V r
56	414.5	52.3	135	2 B32274	Ig heavy chain pre
57	414.5	52.3	141	2 A39276	Ig heavy chain pre
58	413	52.1	166	2 PL0012	Ig heavy chain pre
59	412	52.0	119	2 PH0961	Ig heavy chain V r
60	410	51.7	117	2 S18554	Ig heavy chain V r
61	410	51.7	131	2 S26792	Ig heavy chain V r
62	410	51.7	135	2 PH1492	Ig heavy chain V r
63	410	51.7	151	2 PL0011	Ig heavy chain pre
64	409.5	51.6	122	2 PH0958	Ig heavy chain V r
65	409.5	51.6	128	2 PH0952	Ig heavy chain V r
66	409.5	51.6	137	2 S52445	Ig heavy chain V r
67	409	51.6	135	2 PH1494	Ig heavy chain V r
68	408.5	51.5	139	1 MHMS18	Ig heavy chain pre
69	407.5	51.4	141	2 JL0076	Ig heavy chain pre
70	405.5	51.1	136	2 PH0960	Ig heavy chain V r
71	404.5	51.0	120	2 S31999	Ig heavy chain V r
72	403.5	50.9	116	2 S31698	Ig heavy chain pre
73	403	50.8	125	2 PH0957	Ig heavy chain V r
74	403	50.8	138	2 E32513	Ig heavy chain pre
75	402	50.7	117	1 HVMS8A	Ig heavy chain pre
76	401	50.6	121	2 S20783	Ig heavy chain V r
77	400	50.4	126	2 I44151	Ig heavy chain V r
78	399	50.3	138	2 PH0105	anti-digoxin trans
79	398.5	50.3	137	2 C41287	Ig heavy chain pre
80	398	50.2	98	2 S26919	Ig heavy chain V r
81	398	50.2	135	2 PH0953	Ig heavy chain V r
82	398	50.2	136	2 S35759	BHD9D1.0 protein -
83	395	49.8	121	2 A49590	Ig heavy chain V r
84	394.5	49.7	116	2 PH0959	Ig heavy chain V r
85	394.5	49.7	146	4 S33905	Ig heavy chain pre
86	394	49.7	140	2 PH1499	Ig heavy chain V r
87	394	49.7	140	2 A36194	Ig heavy chain V r
88	392.5	49.5	104	2 PH1665	Ig heavy chain V r
89	392.5	49.5	147	2 PH1561	Ig heavy chain pre
90	391.5	49.4	135	2 A30577	Ig heavy chain pre
91	391.5	49.4	137	1 G2MS43	Ig heavy chain pre
92	391	49.3	98	2 S26938	Ig heavy chain V r
93	390.5	49.2	120	2 PH0962	Ig heavy chain V r
94	389.5	49.1	122	2 PH0887	Ig heavy chain V r
95	389	49.1	131	2 A27472	Ig heavy chain pre
96	389	49.1	138	1 HVMS7	Ig heavy chain pre
97	388	48.9	136	2 PL0208	Ig heavy chain pre
98	387.5	48.8	178	2 S29594	Ig gamma chain (WM
99	387	48.8	125	2 S68170	Ig heavy chain V r
100	387	48.8	129	2 A33548	Ig heavy chain V-1

ALIGNMENTS

RESULT 1

S29257
Ig heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S29257
R:Chouhane, L.; van Spronsen, A.; Breyer, J.; Guglielmi, P.; Strosberg, A.D.
R:J. Biochem. 207, 1115-1121, 1992
A:Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segment
A:Reference number: S29257; MUID:9236264; PMID:1499555
A:Accession: S29257
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <CHO>
A:Cross-references: GB:542403; NID:9253699; PIDN:BA822940.1; PID:G253700
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 63.2%; Score 501; DB 2; Length 148;
Best Local Similarity 62.3%; Pred. No. 2e-38;
Matches 97; Conservative 15; Mismatches 26; Indels 18; Gaps 2;

QY 1 MEWSWFLFLLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MDWTRILFLVAATGAHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
QY 61 GQPEWGWNPYNGNKEFSAKQDRVTFADTSANTAYMELSLRSADTAVYICAR 120
DB 61 GQSLWNGHLSVADGKTKYQKQDRVTFITRDSATAYMEVGLRSEDATVYICAR--- 117

QY 121 YSWDDSPQDNY-----YMDVWGKGTITVIVSS 146
DB 118 -----SPRINWVRGVLITTPFPWDSMGQGLTIVSS 148

RESULT 2

S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R:Friedlander, R.M.; Nussenzeig, M.C.; Leder, P.
Nucleic Acids Res. 19, 4278, 1990
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
A:Reference number: S14683; MUID:90332450; PMID:2115996
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-627 <PRI>
A:Cross-references: EMBL:X17115; NID:933450; PIDN:CAA34971.1; PID:G33451
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin; membrane protein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-627/Product: Ig mu chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 62.5%; Score 496; DB 2; Length 627;
Best Local Similarity 65.1%; Pred. No. 2.5e-37;
Matches 99; Conservative 15; Mismatches 32; Indels 6; Gaps 2;

QY 1 MEWSWFLFLLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MDWTRFLFVAAATGVSQVQLVQSGAEVKKPGSSVKVSQASGGTFFSYALSWVRQAP 60
QY 61 GQPEWGWNPYNGNKEFSAKQDRVTFADTSANTAYMELSLRSADTAVYICAR--- 117
DB 61 GQGLEWNGGIPIFGTANYAKQFGRTITADSTSTAYMELSLRSEDATVYICATGI 120

QY 118 VGPYSWDDSPQDNY---YMDVWGKGTITVIVSS 146
DB 121 LGPYSGWGYNSDYIYGVMDVWGQGTITVIVSS 152

RESULT 3

S18553
Ig heavy chain V region precursor (VI-3b) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18553; S26916
R:Shin, E.K.; Matsuda, F.; Nagasaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Hc
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18553
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62109
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26916
A:Molecule type: DNA
A:Residues: 20-117 <TOM>
A:Cross-references: EMBL:Z12327; NID:932871; PIDN:CAA78197.1; PID:G32872
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-3b) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 60.9%; Score 483; DB 2; Length 117;
Best Local Similarity 75.2%; Pred. No. 6.7e-37;
Matches 88; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 MEWSWFLFLLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MDWTRILFLVAATGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
QY 61 GQPEWGWNPYNGNKEFSAKQDRVTFADTSANTAYMELSLRSADTAVYICAR 117
DB 61 GQLEWNGWINAGNNTKYQKQGRVITRDSASTAYMELSLRSEDATVYICAR 117

RESULT 4

S31600
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31600
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CUI>
A:Cross-references: EMBL:Z14165; NID:930994; PIDN:CAA78534.1; PID:G30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 60.3%; Score 478.5; DB 2; Length 136;
Best Local Similarity 62.3%; Pred. No. 2e-36;
Matches 91; Conservative 18; Mismatches 26; Indels 11; Gaps 2;

QY 1 MEWSWFLFLLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
DB 1 MDWTRILFLVAAATSAHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAT 60


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Db 1 MDWTSLFLVAAATGAHSGVQLVQSGAEVKKPGASVKVSCKASGYTFSTYSGISWVRQAP 60
QY 61 GQPFWMGWINPYNGKFEPAKQDRVTFTADTSANTAYMELSLRSADTAVYICARV-- 118
Db 61 GQGLEWGMWISVYNGDTNYAQNIQGRVTMTDTSTSTAYMELSLRSDDTAVYICARPG 120
QY 119 -----GFSYWDSPQDNYNDVWVGKGTIVVSS 146
Db 121 YCSGGGCGYRGD-----DYWGQGLVTVSS 144

RESULT 9
Ig heavy chain V region precursor (VI-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18552
R:Shin, E.K.; Matsuda, F.; Nagasaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18552
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62107; NID:G37833; PIDN:CAA44017.1; PID:G37834
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-3) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 467; DB 2; Length 117;
Best Local Similarity 72.6%; Pred. No. 1.9e-35;
Matches 85; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 MEWSWVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFSTYSGISWVRQAP 60
Db 1 MDWTSLFLVAAATGAHSGVQLVQSGAEVKKPGASVKVSCKASGYTFSTYSGISWVRQAP 60
QY 61 GQPFWMGWINPYNGKFEPAKQDRVTFTADTSANTAYMELSLRSADTAVYICAR 117
Db 61 GQGLEWGMWISVYNGDTNYAQNIQGRVTMTDTSTSTAYMELSLRSDDTAVYICAR 117

RESULT 10
Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36260
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36260
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-129 <GRI>
A:Cross-references: EMBL:Z18851; NID:G33124; PIDN:CAA79303.1; PID:9939903
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 58.4%; Score 463; DB 2; Length 129;
Best Local Similarity 71.3%; Pred. No. 4.8e-35;
Matches 92; Conservative 8; Mismatches 27; Indels 2; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYSGISWVRQAPGQRFWMGWINPYNGKFE 79
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYSGISWVRQAPGQRFWMGWINPYNGKFE 79
```

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Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYSGISWVRQAPGQGLEWMGWSAYNGNTNY 60
QY 80 SAKFQDRVTFTADTSANTAYMELSLRSADTAVYICAR--VGPSYWDSPQDNYNDVWVG 137
Db 61 AQKLGQRTVMTDTSTSTAYMELSLRSDDTAVYICARSDSGYCSSTSCPYYYNDVWVG 120
QY 138 KGTIVVSS 146
Db 121 KGTIVVSS 129

RESULT 11
Ig heavy chain V region precursor (VI-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18551; S23625
R:Shin, E.K.; Matsuda, F.; Nagasaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18551
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62106; NID:G37831; PIDN:CAA44016.1; PID:G37832
R:Olse, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A.; C
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from tv
A:Reference number: S23623; MUID:92156804; PMID:11740665
A:Accession: S23623
A:Molecule type: DNA
A:Residues: 1-117 <OLE>
A:Cross-references: EMBL:X59704; NID:G32552; PIDN:CAA42225.1; PID:G32553
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 57.1%; Score 453; DB 2; Length 117;
Best Local Similarity 70.1%; Pred. No. 3.5e-34;
Matches 82; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 1 MEWSWVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFSTYSGISWVRQAP 60
Db 1 MDWTSLFLVAAATGAHSGVQLVQSGAEVKKPGASVKVSCKASGYTFSTYSGISWVRQAP 60
QY 61 GQPFWMGWINPYNGKFEPAKQDRVTFTADTSANTAYMELSLRSADTAVYICAR 117
Db 61 GQGLEWGMWISVYNGDTNYAQNIQGRVTMTDTSTSTAYMELSLRSDDTAVYICAR 117

RESULT 12
Ig heavy chain V region (alpha-phOx15) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C:Accession: S19665; S24442
R:Mark, J.D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on pha
A:Reference number: S19663; MUID:92085276; PMID:11748994
A:Accession: S19665
A:Molecule type: mRNA
A:Residues: 1-124 <MAR>
A:Cross-references: EMBL:X61647
R:Jones, P.T.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24442
A:Accession: S24442
A:Molecule type: mRNA
```

A;Residues: 1-40.'GLSGWDGSAITMTQSIDLK' 61-118.'T'.120-124 <JON>
A;Cross-references: EMBL:X61647; NID:g37667; PIDN:CAA43828.1; PID:g1335368
A;Note: the difference for residues 41-60 results from misplacement of 10 bases in the s
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Query Match 57.1%; Score 452.5; DB 2; Length 124;
Best Local Similarity 69.3%; Pred. No. 4.2e-34;
Matches 88; Conservative 13; Mismatches 23; Indels 3; Gaps 1;
QY 20 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAPGQRFEMMGWINPYNGNKEF 79
Db 1 QVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAPGQRFEMMGWINPYNGNKEF 60
QY 80 SAKFDQRTVTTADTSANTAYMELRSADTAVYCARVCPYSWDSQPDNYVMDVWGKG 139
Db 61 AQKLQGRVTMTDTSTSTAYMELRSDDTAVYCVRLLP---KRTATLHYIDVWGKG 117
QY 140 TTVIVSS 146
Db 118 TLTVSS 124
RESULT 13
EIHUND
Ig heavy chain precursor V-I region (Nd) - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000
C;Accession: A93933; A02026
R;Kenten, J.H.; Wolgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A;Title: Cloning and sequence determination of the gene for the human immunoglobulin eps
A;Reference number: A93933; MUID:83065234; PMID:6815656
A;Accession: A93933
A;Molecule type: mRNA
A;Residues: 1-143 <XEN>
R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
A;Reference number: A94418
A;Contents: annotation; partial sequence
A;Note: this epsilon chain was isolated from a myeloma protein
C;Genetics:
A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-143/Product: Ig heavy chain V-I region (Nd) #status predicted <MAT>
F;30-113/Domain: immunoglobulin homology <IMM>
F;16/Modified site: pyroglutamic carboxylic acid (Gln) (in mature form) #status experimen
F;3-111/Disulfide bonds: #status experimental
Query Match 57.1%; Score 452.5; DB 1; Length 143;
Best Local Similarity 58.1%; Pred. No. 4.8e-34;
Matches 86; Conservative 24; Mismatches 31; Indels 7; Gaps 3;
QY 1 MEWSWVFLPFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAP 60
Db 1 MDWT---FLVAATRVHSQTQLVQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAP 56
QY 61 GQRFEMMGWINPYNGNKEFSKFDQRTVTTADTSANTAYMELRSADTAVYCARVCP 120
Db 57 CHGLEWGVINPNSGGTNYAPRQGRVTMTDRASFSTAYMELRSDDSAFVYCAKSP 116
QY 121 YSWDD--SPQDNYVMDVWGKGTTIVSS 146
Db 117 F-MSDYNYFDYSYTLVDWGQGTIVTVSS 143
RESULT 14
S21924

Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S21924; S21923
R;Friedman, D.F.
submitted to the EMBL Data Library, July 1991
A;Reference number: S21923
A;Accession: S21924
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-131 <FRI>
A;Cross-references: EMBL:X60505; NID:g33565; PIDN:CAA43025.1; PID:g33566; EMBL:X60504; N
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
Query Match 56.7%; Score 450; DB 2; Length 131;
Best Local Similarity 68.6%; Pred. No. 7.4e-34;
Matches 83; Conservative 12; Mismatches 26; Indels 0; Gaps 0;
QY 1 MEWSWVFLPFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAP 60
Db 1 MDWTWVILFLVAATGAHSGVQLVPSGAEVKKPGASVKVSQASGYRFSNFIHVRQAP 60
QY 61 GQRFEMMGWINPYNGNKEFSKFDQRTVTTADTSANTAYMELRSADTAVYCARVCP 120
Db 61 GQGLEWGVINPNSGGTNYAQNLRQGRVTMTDTSTSTAYMELRSDDTAVYCARAPG 120
QY 121 Y 121
Db 121 Y 121
RESULT 15
S31680
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31680
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the t
A;Reference number: S31585
A;Accession: S31680
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <CU>
A;Cross-references: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
Query Match 56.6%; Score 449; DB 2; Length 117;
Best Local Similarity 69.2%; Pred. No. 8.2e-34;
Matches 81; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
QY 1 MEWSWVFLPFLSVTTGVHSQVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAP 60
Db 1 MDWTWVILFLVAATGAHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHVRQAP 60
QY 61 GQRFEMMGWINPYNGNKEFSKFDQRTVTTADTSANTAYMELRSADTAVYCAR 117
Db 61 GQGLEWGVINPNSGGTNYAQNLRQGRVTMTDRDTSTSTAYVELSRSDTAVYCAR 117
RESULT 16
A27609
Ig heavy chain precursor V region (I29) - mouse
C;Species: Mus musculus (house mouse)

C>Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
 A/Accession: A27609
 R/Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
 J. Immunol. 140, 1578-1584, 1988
 A/Title: I-29 lymphoma cells express a nonmutated V-H gene before and after H chain switch
 A/Reference number: A27609; MUID:88154467; PMID:3126234
 A/Accession: A27609
 A/Molecule type: DNA
 A/Residues: 1-139 <KLE>
 A/Cross-references: EMBL:M19401; NID:G195441; PIDN:AAA38303.1; PID:G553992
 C/Genetics:
 A/Introns: 16/1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:1-19/DNA: signal sequence #status predicted <SIG>
 F:20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>
 F:34-117/DNA: immunoglobulin homology <IMM>

Query Match 56.6%; Score 448.5; DB 2; Length 139;
 Best Local Similarity 56.8%; Pred. No. 1.1e-33;
 Matches 83; Conservative 25; Mismatches 31; Indels 7; Gaps 1;

QY 1 MEWSWFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
 DB 1 MGWSWIFLLSGTAGVSEVQLQSGPELVKPGASVMSCKASGTFITDYVHWVKQSN 60
 QY 61 GQREPMWGINPYNGKFEKFAQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGP 120
 DB 61 GKSLWIGYINPNKDKGKATLVKSSSTAYVQLNSLTSEDSAVYVCARYS 120
 QY 121 YSWDDSPQDNYMDVWVGKGTIVVSS 146
 DB 121 YSY-----YAMDWGGTIVTVSS 139

RESULT 17
 G2MS11
 Ig gamma-2b chain - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
 A/Accession: G25057; A02157; A26235; A26232; A26233; A53598
 R/Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
 Submitted to the EMBL Data Library, July 1992
 A/Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific
 A/Reference number: S25057
 A/Accession: S25057
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-474 <FIS>
 A/Cross-references: EMBL:X67210; NID:G54826; PIDN:CAA47649.1; PID:G54827
 R/Yanawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
 Nature 283, 786-789, 1980
 A/Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from
 A/Reference number: A02157; MUID:80120716; PMID:6766534
 A/Contents: a allele
 A/Accession: A02157
 A/Molecule type: DNA
 A/Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
 A/Cross-references: GB:J00461
 A/Note: the sequence was determined from the germline gene
 R/Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
 Science 206, 1299-1303, 1979
 A/Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
 A/Reference number: A26235; MUID:80081501; PMID:117548
 A/Contents: MPC 11
 A/Accession: A26235
 A/Molecule type: mRNA
 A/Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
 A/Note: Lys-474 is probably removed posttranslationally
 R/Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
 Science 206, 1303-1306, 1979
 A/Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob
 A/Reference number: A26232; MUID:80081502; PMID:117549

A/Accession: A26232
 A/Molecule type: DNA
 A/Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
 R/Ollo, R.; Rougeon, F.
 Nature 296, 761-763, 1982
 A/Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma
 A/Reference number: A26233; MUID:82173203; PMID:6803173
 A/Contents: b allele
 A/Accession: A26233
 A/Molecule type: DNA
 A/Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
 A/Cross-references: GB:J00461
 R/Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi
 J. Biol. Chem. 269, 12345-12350, 1994
 A/Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
 A/Reference number: A53598; MUID:94216359; PMID:7512967
 A/Accession: A53598
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 234-251 <KIM>
 C/Comment: The a allele sequence is shown.
 C/Genetics:
 A/Introns: 138/1; 236/1; 258/1; 368/1
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai
 C/Superfamily: immunoglobulin C region; immunoglobulin homology
 C/Keywords: alternative splicing; duplication; immunoglobulin; glycoprotein; heterotetramer; immunoglobul
 F:157-222/DNA: immunoglobulin homology <IM1>
 F:236-257/Region: hinge
 F:281-350/DNA: immunoglobulin homology <IM2>
 F:387-454/DNA: immunoglobulin homology <IM3>
 F:152/Disulfide bonds: interchain (to light chain) #status predicted
 F:164-220, 288-348, 394-452/Disulfide bonds: #status predicted
 F:247, 250, 253, 256/Disulfide bonds: interchain (to heavy chain) #status predicted
 F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.1%; Score 444.5; DB 1; Length 474;
 Best Local Similarity 56.8%; Pred. No. 8.8e-33;
 Matches 83; Conservative 19; Mismatches 35; Indels 9; Gaps 1;

QY 1 MEWSWFLFLSVTTGVHSGVQLVQSGAEVKKPGASVKVSQASGYRFSNFIHWVRQAP 60
 DB 1 MGWSWIFLLSGTAGVSEVQLQSGPELVKPGASVMSCKASGTFITDYVHWVKQKP 60
 QY 61 GQREPMWGINPYNGKFEKFAQDRVTFTADTSANTAYMELSLRSADTAVYVCARVGP 120
 DB 61 GKSLWIGYINPNKDKGKATLVKSSSTAYVQLNSLTSEDSAVYVCARYD 120
 QY 121 YSWDDSPQDNYMDVWVGKGTIVVSS 146
 DB 121 YDW-----FAYWGGTIVTVSA 137

RESULT 18
 PS0024
 Ig heavy chain precursor V region (6A4) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
 C/Accession: PS0024
 R/Margat, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
 Gene 74, 335-345, 1988
 A/Title: Cloning and characterization of cDNAs coding for the heavy and light chains of
 A/Reference number: PS0023; MUID:89232725; PMID:3149944
 A/Accession: PS0024
 A/Molecule type: mRNA
 A/Residues: 1-139 <MAR>
 A/Experimental source: strain BALB/c
 C/Comment: this chain is obtained from an IgG2a monoclonal antibody against Pseudomonas
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
 F:1-13/DNA: signal sequence #status predicted <SIG>
 F:20-139/DNA: Ig heavy chain V region #status predicted <IGV>
 F:34-117/DNA: immunoglobulin homology <IMW>

F:20/Modified site: pyroliadone carboxylic acid (Gln) (in mature form) #status predicted

Query Match 55.9%; Score 443.5; DB 2; Length 139;
Best Local Similarity 56.3%; Pred. No. 3.1e-33;
Matches 85; Conservative 21; Mismatches 28; Indels 17; Gaps 2;

QY 1 MEWSVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSQAQSGYRFSNFIHWVRQAP 60
DB 1 MEWHIFLFLSVTAGVHSGVQLVQSGAEVKKPGASVKVSQAQSGYRFSNFIHWVRQAP 60
QY 61 GORFEWGWNPYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYICARVGP 120
DB 61 GQGLEWIGVNPNGYTKYNEKFKGKTLTLDKSSSTAYMQLSLTSDSAVYFCARVY 117
QY 121 YSWDDSPQDNY-----MDVWGKGTIVVSS 146
DB 118 -----SYNYEGAMDYWGQGTIVVSS 139

RESULT 19
S31596
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31596
R:Guisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31596
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <CU1>
A:Cross-references: EMBL:Z14166; NID:g30996; PIDN:CAA78535.1; PID:g30997
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IM>

Query Match 55.8%; Score 442.5; DB 2; Length 132;
Best Local Similarity 58.2%; Pred. No. 3.6e-33;
Matches 85; Conservative 17; Mismatches 29; Indels 15; Gaps 1;

QY 1 MEWSVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSQAQSGYRFSNFIHWVRQAP 60
DB 1 MDWTRILFLVAAATSAHSGVQLVQSGAEVKKPGASVKVSQAQSGYRFSNFIHWVRQAT 60
QY 61 GORFEWGWNPYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYICARVGP 120
DB 61 GQGLEWGWNPNGSNTGVAQKFGQRTVTRNTSISTAYMELSLRAEDTAVYILAKA--- 118
QY 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
DB 119 -----PAMGQGTMTVSS 131

RESULT 20
PH1482
Ig heavy chain V region (clones 36-35[IG] and X7-TG) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1482; PH1495
R:Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1482
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-140 <GU>
A:Experimental source: hybridoma cell
C:Genetics:
A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IM>

Query Match 55.6%; Score 441; DB 2; Length 140;
Best Local Similarity 56.2%; Pred. No. 5.2e-33;
Matches 82; Conservative 28; Mismatches 30; Indels 6; Gaps 1;

QY 1 MEWSVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSQAQSGYRFSNFIHWVRQAP 60
DB 1 MGWSFIFLFLSVTAGVHSGVQLVQSGAEVKKPGASVKVSQAQSGYRFSNFIHWVRQAP 60
QY 61 GORFEWGWNPYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYICARVGP 120
DB 61 GQGLEWIGVNPNGYTKYNEKFKGKTLTLDKSSSTAYMQLSLTSDSAVYFCARVY 120
QY 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
DB 121 YG-----GSYFDYWGQGTIVVSS 140

RESULT 21
PC1155
Ig heavy chain precursor V region (B72.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PC1155
R:Whittle, N.; Adair, J.; Lloyd, C.; Jenkins, L.; Devine, J.; Schlom, J.; Raubitschek, A.
Protein Eng. 1, 499-505, 1987
A:Title: Expression in COS cells of a mouse-human chimaeric B72.3 antibody.
A:Reference number: PC1155; MUID:89220990; PMID:3508296
A:Accession: PC1155
A:Molecule type: mRNA
A:Residues: 1-133 <WH1>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-133/Product: Ig heavy chain V region (B72.3) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IM>

Query Match 55.3%; Score 438.5; DB 2; Length 133;
Best Local Similarity 57.5%; Pred. No. 8.3e-33;
Matches 84; Conservative 23; Mismatches 26; Indels 13; Gaps 2;

QY 1 MEWSVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSQAQSGYRFSNFIHWVRQAP 60
DB 1 MEWSVFLFSLVTTGVHSGVQLVQSGAEVKKPGASVKVSQAQSGYRFSNFIHWVRQAT 60
QY 61 GORFEWGWNPYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVYICARVGP 120
DB 61 GQGLEWIGVNPNGYTKYNEKFKGKTLTLDKSSSTAYMQLSLTSDSAVYFCARVY 117
QY 121 YSWDDSPQDNYMDVWGKGTIVVSS 146
DB 118 -----SYNY-GHWGQGTIVVSS 133

RESULT 22
D33548
Ig heavy chain V-1 region (WIL2) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D33548
R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene ex-
pression in B cell lymphoma.
A:Reference number: A33548; MUID:89345575; PMID:2503826
A:Accession: D33548
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <KIP>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

```

Query Match      55.1%; Score 437; DB 2; Length 123;
Best Local Similarity 66.9%; Pred. No. 1.1e-32;
Matches 85; Conservative 9; Mismatches 29; Indels 4; Gaps 1;

QY 20 QVQLVQSGAEVKKPKQASVKYSCKASGYRPSNFVHHVROAPGQRFHWGWINPINCNEKF 79
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1  QVQLVQSGAEVKKPKQASVKYSCKASGYFTFGHYMHVROAPGQGLGHWGWINPNSGNTY 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 80 SAKFDQRTVTFADTSANTAYMELSLRSADTAVYCARVGPYSWDDS PQDNYIMDVWGSK 139
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 AEKFGQRTVITDTSINTAYMELSLRSDDTAVYCARASVCGYD----CYFFDYWGQG 116
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 140 TTVIVSS 146
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 117 TLTVVSS 123
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

RESULT 23
S19245
IG heavy chain precursor V region (10P1) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: S19245
R/Rirkham, P.M.; Mortari, F.; Newton, J.A.; Schroeder, H.W.
EMBO J. 14, 603-609, 1992
A/Title: Immunoglobulin V(H) clan and family identity predicts variable domain structure
A/Reference number: S19245; MUID:92164649; PMID:1537339
A/Accession: S19245
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-142 <IR>
A/Cross-references: EMBL:X59906; NID:g37791; PIDN:CAA42547.1; PID:g37792
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F.134-117/Domain: immunoglobulin homology <IMM>

[illegible]

RESULT 24
S3z265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C.Accession: S3z265
R.Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A.Title: Human anti-self antibodies with high specificity from phage display libraries.
A.Reference number: S3z256; MUID:93178446; PMID:7679990
A.Accession: S3z265
A.Status: preliminary; nucleic acid sequence not shown
A.Molecule type: mRNA
A.Residues: 1-118 <GR1>
A.Cross-references: EMBL:Z18846; NID:G93121; PID:G939900
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F.15-98/Domain: immunoglobulin homology <IMM>

```

Query Match      55.0%; Score 436.5; DB 2; Length 118;
Best Local Similarity 66.7%; Pred. No. 1.1e-32;
Matches 86; Conservative 11; Mismatches 19; Indels 13; Gaps 2;

QY 20 QVQLVQSGAEVKKPKASVKVSQASGYRFSINFIHWVRQAPGQRFEMWGWINPYNGKEF 79
Db 1 QVQLVQSGAEVKKPKASVKVSCKASGYTFTGYIHWVHVRQAPGQGLEWGWINPNSGGTY 60
QY 80 SAKFQDRVTFTDTSTANTAYMELSLRSADTAVYVCARVGYSDWDSQD--NYVMDVWG 137
Db 61 AQKQFGRVTITRDTASTAYMELSLRSSEDTAVYYCAR-----DFLSGYLDVWG 109

QY 138 KGTITVVS 146
Db 110 QGTLTVSS 118

```

RESULT 25
PH1666
Ig heavy chain V region (clone 6C9) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C/Accession: PH1666
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH1666
A/Molecule type: mRNA
A/Residues: 1-118 <HIL>
A/Experimental source: B cell
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F; 7-90/Domain: immunoglobulin homology <IMM>

Query Match	54.7%	Score 433.5;	DB 2;	Length 118;
Best Local Similarity	70.2%;	Fred. No. 2.1e-32;		
Matches	85; Conservative	12; Mismatches	19; Indels	5; Gaps
QY	28	AEVKKPGASVKVSCQASGYRFESNFIHWVRAPGQSFERNWGINPVGNGKFSAKFQDRV	87	
Db	1	AEVKKPGASVKVSCKASGYTFTSIHWVRAPGQGLEWMGINAGNKTNTAQKFQGRV	60	
QY	88	TFTADTGANTAYMELRSLRSADTAIVYCARGVPYSWDDSPQDNY--MDVWGKGTTIVTS	145	
Db	61	TIETDTASTAYMELLSLRSDTAIVYCARY---TLDDGIKEFYVYGNDVWGQGTIVTS	117	
QY	146	S	146	
Db	118	S	118	

```

RESULT 26
S37483
IG Gamma-2a chain - mouse
C.Species: Mus musculus (house mouse)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C.Accession: S37483
R.Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A.Reference number: S37483
A.Accession: S37483
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-469 <DUC>
A.Cross-references: EMBL:X70423, NID:G406252, PID:CAA49868.1; PID:G406253
C.superfamily: immunoglobulin C region; immunoglobulin homology
C.keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match          54.7%   Score 433.5;   DB 2;   Length 469;
Best Local Similarity 54.4%   Pred. No. 8.6e-32;

```

Query Match	54.7%;	Score 433.5;	DB 2;	Length 469;
Best Local Similarity	54.4%;	Pred. No. 8.6e-32;		

Matches 80; Conservative 27; Mismatches 31; Indels 9; Gaps 2;

QY 1 MEWSWFLFLSVTTGVHSCVQLVQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAP 60
 Db 1 MGWSWIFLLSCTAGVHCQIQQLQSGPELVKPGASVKISCKASGYTFDYINWVKQRP 60

QY 61 GQFEWGWINPNYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVVYCAR-VG 119
 Db 61 GQGLKMGWTPASGNTKYNENFKGATLTVDTSSTAYMQLSSLTSEDVAVVFCARANG 120

QY 120 PYGWDSDSPQDNYMDVWGKGTIVVSS 146
 Db 121 ATA-----TLLDYWGQTLTVSS 139

RESULT 27
 HVHU35
 IG heavy chain precursor V region (V35) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
 C:Accession: S00476; S34013
 R:Matsuda, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Fukuhara
 EMBL J. 7, 1047-1051, 1988
 A>Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain loc
 A:Reference number: S00476; MUID:88296408; PMID:2841108
 A:Accession: S00476
 A:Molecule type: DNA
 A:Residues: 1-117 <NATS>
 A:Cross-references: EMBL:X07448; NID:g33104; PIDN:CAB56703.1; PID:g6002173
 A>Note: the authors translated the codon AGT for residue 89 as Met
 R:Marlette, X.; Tsapis, A.; Brouet, J.C.
 Eur. J. Immunol. 23, 846-851, 1993
 A>Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
 A:Reference number: S34001; MUID:93209281; PMID:7681398
 A:Accession: S34013
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 20-116 <MAR>
 C:Genetics:
 A:Gene: GDB:IGHV6
 A:Cross-references: GDB:128528; OMIM:147070
 A:Map position: 14q32.33-14q32.33
 A:Introns: 16/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: IG heavy chain V region (V35) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 54.6%; Score 433; DB 1; Length 117;
 Best Local Similarity 68.4%; Pred. No. 2.3e-32;
 Matches 80; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

QY 1 MEWSWFLFLSVTTGVHSCVQLVQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAP 60
 Db 1 MDWTRFLFLVAATGAHSCVQLVQSGAEVKKPGASVKISCKASGYTFDYINWVKQRP 60

QY 61 GQFEWGWINPNYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVVYCAR 117
 Db 61 GQGLEWGWINPNSGGTNAQKFGQVTSRTDTSSTAYMELSLRSDDTVVYCAR 117

RESULT 28
 C33548
 IG heavy chain V-1 region (783) - human
 C:Species: Homo sapiens (man)
 C>Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
 C:Accession: C33548
 R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
 A>Title: Developmentally restricted immunoglobulin heavy chain variable region gene exp
 A:Reference number: A33548; MUID:89345575; PMID:2503826
 A:Accession: C33548

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
 A:Molecule type: DNA
 A:Residues: 1-133 <KIP>
 A:Experimental source: the sequence was determined from the differentiated gene
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 54.6%; Score 433; DB 2; Length 133;
 Best Local Similarity 66.9%; Pred. No. 2.6e-32;
 Matches 89; Conservative 11; Mismatches 27; Indels 6; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAFQGFEMWGWINPNYNGNKEF 79
 Db 1 QVQLVQSGAEVKKPGSSVKVSKASGTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 60

QY 80 SAKFQDRVTFTADTSANTAYMELSLRSADTAVVYCAR---VGPVSNDDSPQDNY---M 133
 Db 61 AQKQGRVTITADSTSTAYMELSLRSADTAVVYCARGTGILGPYSSGWYNSDYIYVGM 120

QY 134 DWGKGTTIVVSS 146
 Db 121 DWGQGTIVTVSS 133

RESULT 29
 H32513
 IG heavy chain precursor V region (BXW16) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
 C:Accession: H32513
 R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; I
 J. Clin. Invest. 82, 852-860, 1988
 A>Title: Immunoglobulin kappa light chain variable region gene complex organization and
 A:Reference number: A94689; MUID:88331394; PMID:3138286
 A:Accession: H32513
 A:Molecule type: DNA
 A:Residues: 1-137 <KOP>
 A:Cross-references: GB:M20831; NID:g196949; PIDN:AAA38848.1; PID:g196950
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 54.5%; Score 432.5; DB 2; Length 137;
 Best Local Similarity 54.7%; Pred. No. 3e-32;
 Matches 81; Conservative 25; Mismatches 29; Indels 13; Gaps 2;

QY 1 MEWSWFLFLSVTTGVHSCVQLVQSGAEVKKPGASVKVSQCASGYRFSNFIHWVRQAP 60
 Db 1 MGWSWIFLLSVTAGVHSEIQLQSGAEVKKPGASVKISCKASGYSTGYNNWVKQSH 60

QY 61 GQFEWGWINPNYNGNKEFSKAFQDRVTFTADTSANTAYMELSLRSADTAVVYCARVGP 120
 Db 61 GKSLEWIGINPNYGGTSYNGKFKGATLTVDKSSSTAYMQLNSLTSEDSAVVYCAR--- 117

QY 121 YSWDDSPQDNY---YMDVWGKGTIVVSS 146
 Db 118 -----KNYSSFDYWGQTLTVSS 137

RESULT 30
 A32483
 IG heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
 C:Accession: A32483
 R:Larlick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, C.
 Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
 A>Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells usir
 A:Reference number: A32483; MUID:89273586; PMID:2499327
 A:Accession: A32483
 A>Status: preliminary
 A:Molecule type: mRNA

A;Residues: 1-142 <LAR>
A;Cross-references: GB:M26463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>
Query Match 54.5%; Score 432; DB 2; Length 142;
Best Local Similarity 59.1%; Pred. No. 3.5e-32;
Matches 88; Conservative 10; Mismatches 25; Indels 26; Gaps 2;
Qy 11 LSVTTGVHSQVLVQSGAEVKKPGASVKVSCASGYRFSNFVIHWVRQAPGQRFEMGWI 70
Db 2 LAVAPGAHSQVLVQSGAEVKKPGASVKVSCASGYTFNYYMHWVRQAPGQGLEWVGII 61
Qy 71 NPYNGNKFSAKPDQDRVTFTADTSANTAYMELSLRSADTAVYCAR----- 117
Db 62 NPSGNTNYAQKFGQGVTVTRDTSTSTVYMELSLSRSEDVAVYCAREKLATTIFGLII 121
Qy 118 VGPYSWDDSPQDNYMDVMGKGTIVVSS 146
Db 122 TG-----MDYWGQGLTVVSS 137

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Job time : 15.0593 secs